

Result No.	Score	Query Match	Length	DB ID	Description
SUMMARIES					
1	557	100.0	107	3	US-09-851-614-2
2	557	100.0	107	4	US-10-035-631-2
3	557	100.0	107	5	US-10-169-144-8
4	557	100.0	107	5	US-10-901-191-6
5	557	100.0	233	5	US-10-169-144-6
6	557	100.0	233	5	US-10-903-191-6
7	557	100.0	411	5	US-10-769-144-12
8	557	100.0	411	5	US-10-903-191-12
9	538	96.6	107	3	US-09-948-939-13
10	538	96.6	107	6	US-11-040-816-13
11	538	96.6	108	4	US-10-108-901-13
12	538	96.6	214	4	US-10-408-901-44
13	535	96.4	107	5	US-10-891-658-88
14	535	96.1	107	4	US-10-703-714-4
15	535	96.1	107	4	US-10-703-714-8
16	535	96.1	236	5	US-10-858-186-20
17	535	96.1	107	4	US-10-703-714-16
18	531	95.3	107	5	US-10-815-449-6
19	531	95.3	107	6	US-11-009-731-91
20	531	95.3	107	6	US-11-102-403-13
21	530	95.2	107	4	US-10-221-529-4
22	529	95.0	107	5	US-10-815-449-2
23	529	95.0	107	5	US-10-815-449-4
24	529	95.0	108	3	US-09-920-263A-8
25	529	95.0	108	5	US-10-912-994-8
26	529	95.0	108	5	US-10-975-883-8
27	529	95.0	108	5	US-10-975-740A-8
ALIGMENTS					
28	529	95.0	108	5	US-10-975-708-8
29	526	94.4	107	6	US-11-102-403-5
30	526	94.4	107	6	US-11-102-403-7
31	524	94.1	108	4	US-10-408-901-12
32	524	94.1	214	4	US-10-408-901-16
33	522	93.7	107	6	US-11-102-403-15
34	521	93.5	128	4	US-10-389-221-12
35	521	93.5	128	5	US-10-909-851-16
36	519	93.2	107	4	US-10-338-366-12
37	508	91.2	107	5	US-10-727-155-12
38	508	91.2	129	5	US-10-910-901-20
39	506	90.8	107	4	US-10-941-880-43
40	506	90.8	107	4	US-10-041-860-18
41	506	90.8	107	4	US-10-665-383-64
42	505	90.7	127	4	US-10-395-894-25
43	505	90.7	127	4	US-10-695-667-35
44	505	90.7	127	5	US-10-976-352-25
45	504	90.5	107	5	US-10-727-155-12

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Published Applications AA Main:*
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2: /cgn2_6/podata/1/pubpaas/US08_PUBCOMB.pep:*
3: /cgn2_6/podata/1/pubpaas/US09_PUBCOMB.pep:*
4: /cgn2_6/podata/1/pubpaas/US10_PUBCOMB.pep:*
5: /cgn2_6/podata/1/pubpaas/US10_PUBCOMB.pep:*
6: /cgn2_6/podata/1/pubpaas/US11_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
ALIGMENTS					
1	557	100.0	107	3	US-09-851-614-2
2	557	100.0	107	4	US-10-035-631-2
3	557	100.0	107	5	US-10-169-144-8
4	557	100.0	107	5	US-10-901-191-6
5	557	100.0	233	5	US-10-169-144-6
6	557	100.0	233	5	US-10-903-191-6
7	557	100.0	411	5	US-10-769-144-12
8	557	100.0	411	5	US-10-903-191-12
9	538	96.6	107	3	US-09-948-939-13
10	538	96.6	107	6	US-11-040-816-13
11	538	96.6	108	4	US-10-108-901-13
12	538	96.6	214	4	US-10-408-901-44
13	535	96.4	107	5	US-10-891-658-88
14	535	96.1	107	4	US-10-703-714-4
15	535	96.1	107	4	US-10-703-714-8
16	535	96.1	236	5	US-10-858-186-20
17	535	96.1	107	4	US-10-703-714-16
18	531	95.3	107	5	US-10-815-449-6
19	531	95.3	107	6	US-11-009-731-91
20	531	95.3	107	6	US-11-102-403-13
21	530	95.2	107	4	US-10-221-529-4
22	529	95.0	107	5	US-10-815-449-2
23	529	95.0	107	5	US-10-815-449-4
24	529	95.0	108	3	US-09-920-263A-8
25	529	95.0	108	5	US-10-912-994-8
26	529	95.0	108	5	US-10-975-883-8
27	529	95.0	108	5	US-10-975-740A-8

ALIGMENTS**GENERAL INFORMATION:**

; GENERAL INFORMATION:

; APPLICANT: Deo, Yashwant M.

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC

; FILE REFERENCE: MXI-166

; CURRENT APPLICATION NUMBER: US-09/851-614-2

; CURRENT FILING DATE: 2001-05-08

; PRIORITY FILING DATE: 2000-05-08

; PRIOR APPLICATION NUMBER: USSN 60/233,126

; PRIOR FILING DATE: 2000-09-07

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 2

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Homo sapiens

; SEQ ID: 09-851-614-2

; QUERY MATCH

100.0%

Score 557;

DB 3;

Length 107;

; BEST LOCAL SIMILARITY

100.0%

; PRED. NO.

2.6e-42;

; MATCHES

0;

; INDELS

0;

; GAPS

0;

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i PRIOR FILING DATE: 2001-03-08
 i PRIOR APPLICATION NUMBER: USSN 60/203,126
 i PRIOR FILING DATE: 2000-05-08
 i PRIOR APPLICATION NUMBER: USSN 60/230,739
 i PRIOR FILING DATE: 2000-09-07
 i NUMBER OF SEQ ID NOS: 9
 i SOFTWARE: FastSEQ for Windows Version 4.0
 i SEQ ID NO: 2
 i LENGTH: 107
 i TYPE: PRT
 i ORGANISM: Homo sapiens
 us-10-035-637-2

Query Match 100.0%; Score 557; DB 4; Length 107;
 Best Local Similarity 100.0%; Pred. No. 2.6e-42; Indels 0; Gaps 0;
 Matches 107; Conservative 0; N mismatches 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRSRMLWYQQKPEAKPSLIVAAASSLQSGVPS 60
 Db 1 DIQMTQSPSSLSASVGDRVTITCRASQISRSRMLWYQQKPEAKPSLIVAAASSLQSGVPS 60

Qy 61 RFSGSGSGTDFLTISGLQPEDFATYQQYNNSPRTFGGTKVIEK 107
 Db 61 RFSGSGSGTDFLTISGLQPEDFATYQQYNNSPRTFGGTKVIEK 107

RESULT 3
us-10-769-144-8

i Sequence 8, Application US/10769144
 i Publication No. US20040248215A1
 i GENERAL INFORMATION:
 i APPLICANT: Keller, Tibor
 i ENDRES, Michael
 i APPLICANT: He, Lizhen
 i APPLICANT: Ramakrishna, Venky
 i TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
 i TITLE OF INVENTION: THEREFOR
 i FILE REFERENCE: MXI-301
 i CURRENT APPLICATION NUMBER: US/10/769,144
 i CURRENT FILING DATE: 2004-01-10
 i PRIOR APPLICATION NUMBER: 60/443979
 i PRIOR FILING DATE: 2003-01-31
 i NUMBER OF SEQ ID NOS: 22
 i SOFTWARE: FastSEQ for Windows Version 4.0
 i SEQ ID NO: 8
 i LENGTH: 107
 i TYPE: PRT
 i ORGANISM: Homo sapiens
 us-10-769-144-8

Query Match 100.0%; Score 557; DB 5; Length 107;
 Best Local Similarity 100.0%; Pred. No. 2.6e-42; Indels 0; Gaps 0;
 Matches 107; Conservative 0; N mismatches 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRSRMLWYQQKPEAKPSLIVAAASSLQSGVPS 60
 Db 1 DIQMTQSPSSLSASVGDRVTITCRASQISRSRMLWYQQKPEAKPSLIVAAASSLQSGVPS 60

Qy 61 RFSGSGSGTDFLTISGLQPEDFATYQQYNNSPRTFGGTKVIEK 107
 Db 61 RFSGSGSGTDFLTISGLQPEDFATYQQYNNSPRTFGGTKVIEK 107

RESULT 4
us-10-903-191-8

i Sequence 8, Application US/10903191
 i Publication No. US2005180983A1
 i GENERAL INFORMATION:
 i APPLICANT: Keller, Tibor
 i ENDRES, Michael
 i APPLICANT: He, Lizhen
 i APPLICANT: Ramakrishna, Venky
 i TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES

Query Match 100.0%; Score 557; DB 5; Length 233;
 Best Local Similarity 100.0%; Pred. No. 5.6e-42; Indels 0; Gaps 0;
 Matches 107; Conservative 0; N mismatches 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRSRMLWYQQKPEAKPSLIVAAASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRSRMLWYQQKPEAKPSLIVAAASSLQSGVPS 79

Qy 61 RFSGSGSGTDFLTISGLQPEDFATYQQYNNSPRTFGGTKVIEK 107
 Db 80 RFSGSGSGTDFLTISGLQPEDFATYQQYNNSPRTFGGTKVIEK 126

RESULT 5
us-10-769-144-6

i Sequence 6, Application US/10769144
 i Publication No. US20040248215A1
 i GENERAL INFORMATION:
 i APPLICANT: Keller, Tibor
 i ENDRES, Michael
 i APPLICANT: He, Lizhen
 i APPLICANT: Ramakrishna, Venky
 i TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
 i TITLE OF INVENTION: THEREFOR
 i FILE REFERENCE: MXI-301
 i CURRENT APPLICATION NUMBER: US/10/769,144
 i CURRENT FILING DATE: 2004-01-30
 i PRIOR APPLICATION NUMBER: 60/443979
 i PRIOR FILING DATE: 2003-01-31
 i NUMBER OF SEQ ID NOS: 32
 i SOFTWARE: FastSEQ for Windows Version 4.0
 i SEQ ID NO: 6
 i LENGTH: 233
 i TYPE: PRT
 i ORGANISM: Homo sapiens
 us-10-769-144-6

Query Match 100.0%; Score 557; DB 5; Length 233;
 Best Local Similarity 100.0%; Pred. No. 5.6e-42; Indels 0; Gaps 0;
 Matches 107; Conservative 0; N mismatches 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRSRMLWYQQKPEAKPSLIVAAASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRSRMLWYQQKPEAKPSLIVAAASSLQSGVPS 79

Qy 61 RFSGSGSGTDFLTISGLQPEDFATYQQYNNSPRTFGGTKVIEK 107
 Db 80 RFSGSGSGTDFLTISGLQPEDFATYQQYNNSPRTFGGTKVIEK 126

RESULT 6
us-10-903-191-6

i Sequence 6, Application US/10903191
 i Publication No. US2005180983A1
 i GENERAL INFORMATION:
 i APPLICANT: Keller, Tibor
 i ENDRES, Michael
 i APPLICANT: He, Lizhen
 i APPLICANT: Ramakrishna, Venky
 i TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES

APPLICANT: He, Lizhen
 APPLICANT: Ramakrishna, Venky
 TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
 TITLE OF INVENTION: THEREFOR
 CURRENT APPLICATION NUMBER: US/10/903,191
 CURRENT FILING DATE: 2004-07-30
 PRIOR APPLICATION NUMBER: 60/443979
 PRIOR FILING DATE: 2004-01-30
 PRIORITY NUMBER: 60/443979
 PRIORITY FILING DATE: 2003-01-31
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 6
 LENGTH: 233
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-903-191-6

Query Match 100.0%; Score 557; DB 5; Length 233;
 Best Local Similarity 100.0%; Pred. No. 5.6e-42;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRWLAVYQQKPKBAPKSLIYAAASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRWLAVYQQKPKBAPKSLIYAAASSLQSGVPS 79

Qy 61 RFSGSGSGTDFLTISGLQPEDFATYYCQQTNSYPTFGQGTKVIEK 107
 Db 80 RFSGSGSGTDFLTISGLQPEDFATYYCQQTNSYPTFGQGTKVIEK 126

RESULT 7
 US-10-769-144-12
 Sequence 12, Application US/10769144
 Publication No. US20040248215A1
 GENERAL INFORMATION:
 APPLICANT: Keler, Tibor
 APPLICANT: Endres, Michael
 APPLICANT: He, Lizhen
 APPLICANT: Ramakrishna, Venky
 TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
 TITLE OF INVENTION: THEREFOR
 FILE REFERENCE: MXI-301CP
 CURRENT APPLICATION NUMBER: US/10/769,144
 CURRENT FILING DATE: 2004-01-30
 PRIOR APPLICATION NUMBER: 60/443979
 PRIOR FILING DATE: 2003-01-31
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 12
 LENGTH: 411
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-769-144-12

Query Match 100.0%; Score 557; DB 5; Length 411;
 Best Local Similarity 100.0%; Pred. No. 1e-41;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRWLAVYQQKPKBAPKSLIYAAASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRWLAVYQQKPKBAPKSLIYAAASSLQSGVPS 79

Qy 61 RFSGSGSGTDFLTISGLQPEDFATYYCQQNSYPTFGQGTKVIEK 107
 Db 80 RFSGSGSGTDFLTISGLQPEDFATYYCQQNSYPTFGQGTKVIEK 126

GENERAL INFORMATION:
 APPLICANT: Keler, Tibor
 APPLICANT: Endres, Michael
 APPLICANT: He, Lizhen
 APPLICANT: Ramakrishna, Venky
 TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
 TITLE OF INVENTION: THEREFOR
 FILE REFERENCE: MXI-301CP
 CURRENT APPLICATION NUMBER: US/10/903,191
 CURRENT FILING DATE: 2004-07-30
 PRIOR APPLICATION NUMBER: 10/769144
 PRIOR FILING DATE: 2004-01-30
 PRIOR APPLICATION NUMBER: 60/443979
 PRIOR FILING DATE: 2003-01-31
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 12
 LENGTH: 411
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-903-191-12

Query Match 100.0%; Score 557; DB 5; Length 411;
 Best Local Similarity 100.0%; Pred. No. 1e-41;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRWLAVYQQKPKBAPKSLIYAAASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRWLAVYQQKPKBAPKSLIYAAASSLQSGVPS 79

Qy 61 RFSGSGSGTDFLTISGLQPEDFATYYCQQNSYPTFGQGTKVIEK 107
 Db 80 RFSGSGSGTDFLTISGLQPEDFATYYCQQNSYPTFGQGTKVIEK 126

RESULT 9
 US-09-948-939-13
 Sequence 13, Application US/09948939
 Publication No. US2002008604A1
 GENERAL INFORMATION:
 APPLICANT: Kortman, Alan J.
 APPLICANT: Halk, Edward L.
 APPLICANT: Lonberg, Nils
 APPLICANT: Medarex, Inc.
 TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses
 FILE REFERENCE: 01463-01520US
 CURRENT APPLICATION NUMBER: US/09/948,939
 CURRENT FILING DATE: 2003-12-18
 PRIOR APPLICATION NUMBER: US 60/150,452
 PRIOR FILING DATE: 1999-08-24
 PRIOR APPLICATION NUMBER: 09/644,668
 PRIOR FILING DATE: 2000-03-24
 NUMBER OF SEQ ID NOS: 41
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 13
 LENGTH: 107
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURER: OTHER INFORMATION: Light chain variable region predicted sequence for
 OTHER INFORMATION: 1E2 from Vκ L-15
 OTHER INFORMATION: 1E2 from Vκ L-15
 US-09-948-939-13

Query Match 96.6%; Score 538; DB 3; Length 107;
 Best Local Similarity 97.2%; Pred. No. 1.3e-40;
 Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRWLAVYQQKPKBAPKSLIYAAASSLQSGVPS 60
 Db 1 DIQMTQSPSSLSASVGDRVTITCRASQISRWLAVYQQKPKBAPKSLIYAAASSLQSGVPS 60

Qy 61 RFSGSGSGTDFLTISGLQPEDFATYYCQQNSYPTFGQGTKVIEK 107
 Db 80 RFSGSGSGTDFLTISGLQPEDFATYYCQQNSYPTFGQGTKVIEK 126

RESULT 8
 US-10-903-191-12
 Sequence 12, Application US/10903191
 Publication No. US20050180983A1

Db 61 RFSGSGSGTDFLTISLQPEDFATYYCQQYNSYPPTFGQGTKEIK 107 Qy 1 D1QMTQSPSSLSASVGDRVITCRASOGISRMLAWYQKPEKAPSLIYAASSLQSGVPS 60
 RESULT 10 Db 1 D1QMTQSPSSLSASVGDRVITCRASOGISRMLAWYQKPEKAPSLIYAASSLQSGVPS 60
 US-11-040-846-13
 / Sequence 13, Application US/11040846
 / Publication No. US20050201994A1
 / GENERAL INFORMATION:
 / APPLICANT: Korman, Alan J.
 / APPLICANT: Halk, Edward L.
 / APPLICANT: Lonberg, Nils
 / APPLICANT: Medarex, Inc.
 / TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses
 / FILE REFERENCE: 01463-010520US
 / CURRENT APPLICATION NUMBER: US/11/040, 846
 / CURRENT FILING DATE: 2005-01-20
 / PRIORITY NUMBER: US/09/948, 939
 / PRIOR APPLICATION NUMBER: US/09/093/07
 / PRIOR FILING DATE: 2001-09-24
 / PRIORITY NUMBER: US 60/150, 452
 / PRIOR FILING DATE: 1999-08-24
 / PRIOR APPLICATION NUMBER: 09/644, 666
 / PRIOR FILING DATE: 2000-08-24
 / NUMBER OF SEQ ID NOS: 41
 / SOFTWARE: Patentin Ver. 2.1
 / SEQ ID NO: 13
 / LENGTH: 107
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / FEATURE:
 / OTHER INFORMATION: light chain variable region predicted sequence for:
 / OTHER INFORMATION: 1E2 from Vκ L-15
 / US-11-040-846-13

Query Match 96.6%; Score 538; DB 6; Length 107;
 Best Local Similarity 97.2%; Pred. No. 1.3e-40;
 Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1 D1QMTQSPSSLSASVGDRVITCRASOGISRMLAWYQKPEKAPSLIYAASSLQSGVPS 60
 Db 1 D1QMTQSPSSLSASVGDRVITCRASOGISRMLAWYQKPEKAPSLIYAASSLQSGVPS 60

Qy 61 RFSGSGSGTDFLTISLQPEDFATYYCQQYNSYPPTFGQGTKEIK 107
 Db 61 RFSGSGSGTDFLTISLQPEDFATYYCQQYNSYPPTFGQGTKEIK 107

RESULT 11
 US-10-408-901-20
 / Sequence 20, Application US/10408901
 / Publication No. US2004023313A1
 / GENERAL INFORMATION:
 / APPLICANT: Boyle, William
 / APPLICANT: Huang, Haichun
 / APPLICANT: Elliot, Robin
 / APPLICANT: Sullivan, John
 / APPLICANT: Medlock, Eugene
 / APPLICANT: Martin, Francis
 / APPLICANT: Inoue, Heather
 / APPLICANT: Zhang, Tie J.
 / APPLICANT: Martini, Frank
 / TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
 / FILE REFERENCE: MBHB 01-1145-A
 / CURRENT APPLICATION NUMBER: US/10/408, 901
 / CURRENT FILING DATE: 2003-04-07
 / NUMBER OF SEQ ID NOS: 76
 / SOFTWARE: Patentin version 3.0
 / SEQ ID NO: 20
 / LENGTH: 108
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / US-10-408-901-20

Query Match 96.6%; Score 538; DB 4; Length 108;
 Best Local Similarity 97.2%; Pred. No. 1.3e-40;
 Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 D1QMTQSPSSLSASVGDRVITCRASOGISRMLAWYQKPEKAPSLIYAASSLQSGVPS 60
 Db 1 D1QMTQSPSSLSASVGDRVITCRASOGISRMLAWYQKPEKAPSLIYAASSLQSGVPS 60

Qy 61 RFSGSGSGTDFLTISLQPEDFATYYCQQYNSYPPTFGQGTKEIK 107
 Db 61 RFSGSGSGTDFLTISLQPEDFATYYCQQYNSYPPTFGQGTKEIK 107

RESULT 12
 US-10-408-901-44
 / Sequence 44, Application US/10408901
 / Publication No. US2004023313A1
 / GENERAL INFORMATION:
 / APPLICANT: Boyle, William
 / APPLICANT: Huang, Haichun
 / APPLICANT: Elliot, Robin
 / APPLICANT: Sullivan, John
 / APPLICANT: Medlock, Eugene
 / APPLICANT: Martin, Francis
 / APPLICANT: Inoue, Heather
 / APPLICANT: Zhang, Tie J.
 / APPLICANT: Martini, Frank
 / TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
 / FILE REFERENCE: MBHB 1-1145-A
 / CURRENT APPLICATION NUMBER: US/10/408, 901
 / CURRENT FILING DATE: 2003-04-07
 / NUMBER OF SEQ ID NOS: 76
 / SOFTWARE: Patentin version 3.0
 / SEQ ID NO: 44

Query Match 96.6%; Score 538; DB 4; Length 214;
 Best Local Similarity 97.2%; Pred. No. 2.6e-40;
 Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 D1QMTQSPSSLSASVGDRVITCRASOGISRMLAWYQKPEKAPSLIYAASSLQSGVPS 60
 Db 1 D1QMTQSPSSLSASVGDRVITCRASOGISRMLAWYQKPEKAPSLIYAASSLQSGVPS 60

Qy 61 RFSGSGSGTDFLTISLQPEDFATYYCQQYNSYPPTFGQGTKEIK 107
 Db 61 RFSGSGSGTDFLTISLQPEDFATYYCQQYNSYPPTFGQGTKEIK 107

RESULT 13
 US-10-891-658-88
 / Sequence 88, Application US/10891658
 / Publication No. US20050074821A1
 / GENERAL INFORMATION:
 / APPLICANT: Kenneth, Wild
 / APPLICANT: Treanor, James
 / APPLICANT: Huang, Haichun
 / APPLICANT: Inoue, Heather
 / APPLICANT: Zhang, Tie J.
 / APPLICANT: Martini, Frank
 / TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies
 / FILE REFERENCE: 02-1240
 / CURRENT APPLICATION NUMBER: US/10/891, 658
 / CURRENT FILING DATE: 2004-07-15
 / PRIOR APPLICATION NUMBER: US 60/487, 431
 / PRIOR FILING DATE: 2003-07-15
 / NUMBER OF SEQ ID NOS: 138
 / SOFTWARE: Patentin version 3.0
 / SEQ ID NO: 88
 / LENGTH: 107
 / TYPE: PRT
 / ORGANISM: homo sapien
 / US-10-891-658-88

Query Match 96.4%; Score 537; DB 5; Length 107;
 Best Local Similarity 97.2%; Pred. No. 1.6e-40;
 Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLASVGDRVTITCRASQISRWLAWYQQPEKAPSLIYASSLQSGVPS 60
 Db 1 DIQMTQSPSSLASVGDRVTITCRASQISRWLAWYQQPEKAPSLIYASSLQSGVPS 60
 Qy 61 RFSGSGSGTDFLTISCLQPEDFATYYCQQNSYPTFGQGTKEIK 107
 Db 61 RFSGSGSGTDFLTISCLQPEDFATYYCQQNSYPTFGQGTKEIK 107

Query completed: December 3, 2005, 14:17:34
 Job time : 147.743 secs

RESULT 14
 US-10-703-714-4
 i Sequence 4, Application US/10703714
 i Publication No. US20040170630A1
 i GENERAL INFORMATION:
 i APPLICANT: Huang, Haichun
 i APPLICANT: Holmes, Steven
 i APPLICANT: Mason, Sean
 i TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HEPARANASE
 i FILE REFERENCE: MXI-294
 i CURRENT APPLICATION NUMBER: US/10/703,714
 i CURRENT FILING DATE: 2003-11-07
 i PRIOR APPLICATION NUMBER: 60/424803
 i PRIOR FILING DATE: 2002-11-07
 i NUMBER OF SEQ ID NOS: 64
 i SOFTWARE: FastSEQ for Windows Version 4.0
 i SEQ ID NO 4
 i LENGTH: 107
 i TYPE: PRT
 i ORGANISM: Homo sapiens
 i US-10-703-714-4

Query Match 96.1%; Score 535; DB 4; Length 107;
 Best Local Similarity 96.3%; Pred. No. 2.4e-40;
 Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLASVGDRVTITCRASQISRWLAWYQQPEKAPSLIYASSLQSGVPS 60
 Db 1 DIQMTQSPSSLASVGDRVTITCRASQISRWLAWYQQPEKAPSLIYASSLQSGVPS 60
 Qy 61 RFSGSGSGTDFLTISCLQPEDFATYYCQQNSYPTFGQGTKEIK 107
 Db 61 RFSGSGSGTDFLTISCLQPEDFATYYCQQNSYPTFGQGTKEIK 107

RESULT 15
 US-10-703-714-8
 i Sequence 8, Application US/10703714
 i Publication No. US20040170630A1
 i GENERAL INFORMATION:
 i APPLICANT: Huang, Haichun
 i APPLICANT: Holmes, Steven
 i APPLICANT: Mason, Sean
 i TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HEPARANASE
 i FILE REFERENCE: MXI-294
 i CURRENT APPLICATION NUMBER: US/10/703,714
 i CURRENT FILING DATE: 2003-11-07
 i PRIOR APPLICATION NUMBER: 60/424803
 i PRIOR FILING DATE: 2002-11-07
 i NUMBER OF SEQ ID NOS: 64
 i SOFTWARE: FastSEQ for Windows Version 4.0
 i SEQ ID NO 8
 i LENGTH: 107
 i TYPE: PRT
 i ORGANISM: Homo sapiens
 i US-10-703-714-8

Query Match 96.1%; Score 535; DB 4; Length 107;
 Best Local Similarity 96.3%; Pred. No. 2.4e-40;
 Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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OM protein - protein search, using SW model

Run on: December 3, 2005, 13:48:29 ; Search time 6.11429 Seconds
 Perfect score: 557 (without alignments)
 Sequence: 1 DIQMTQSPSSLSASVGDRVTI...CQQYNSYPRTFGGTKVEIK 107

Title: US-10-769-144-8

Scoring table: BLOSUM62 Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

Published Applications AA_New:
 1: /cgn2_6/podata/1/pubpaas/US09_NEW_PUB.PEP:
 2: /cgn2_6/podata/1/pubpaas/US07_NEW_PUB.PEP:
 3: /cgn2_6/podata/1/pubpaas/US06_NEW_PUB.PEP:
 4: /cgn2_6/podata/1/pubpaas/US08_NEW_PUB.PEP:
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 7: /cgn2_6/podata/1/pubpaas/US11_NEW_PUB.PEP:
 8: /cgn2_6/podata/1/pubpaas/US60_NEW_PUB.PEP:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	4.95	88.9	244	7 US-11-054-515-1881 Sequence 1881, AP
2	4.86	87.3	236	7 US-11-054-515-1881 Sequence 1881, AP
3	4.84	86.9	95	7 US-11-084-554-126 Sequence 126, APP
4	4.84	86.9	107	7 US-11-084-554-1 Sequence 1, APP
5	4.84	86.9	236	7 US-11-054-515-1882 Sequence 48, APP
6	4.83	86.7	244	7 US-11-054-515-82 Sequence 82, APP
7	4.83	86.7	244	7 US-11-054-515-261 Sequence 261, APP
8	4.79	86.0	95	7 US-11-054-669-62 Sequence 62, APP
9	4.79	86.0	113	7 US-11-056-074-53 Sequence 53, APP
10	4.79	86.0	244	7 US-11-054-515-164 Sequence 164, APP
11	4.78	85.8	244	7 US-11-054-515-280 Sequence 280, APP
12	4.77	85.6	239	7 US-11-054-515-1882 Sequence 1882, APP
13	4.77	85.6	239	7 US-11-054-515-1922 Sequence 1922, APP
14	4.77	85.6	241	7 US-11-054-515-1889 Sequence 1889, APP
15	4.77	85.6	241	7 US-11-054-515-1901 Sequence 1901, APP
16	4.77	85.6	243	7 US-11-054-515-1883 Sequence 1983, APP
17	4.77	85.6	243	7 US-11-054-515-1935 Sequence 1935, APP
18	4.77	85.6	243	7 US-11-054-515-1945 Sequence 1945, APP
19	4.77	85.6	243	7 US-11-054-515-2063 Sequence 2063, APP
20	4.77	85.6	245	7 US-11-054-515-1900 Sequence 1900, APP
21	4.77	85.6	245	7 US-11-054-515-1902 Sequence 1902, APP
22	4.77	85.6	246	7 US-11-054-515-1920 Sequence 1920, APP
23	4.77	85.6	246	7 US-11-054-515-2062 Sequence 2062, APP
24	4.77	85.6	247	7 US-11-054-515-969 Sequence 969, APP
25	4.77	85.6	247	7 US-11-054-515-1177 Sequence 1177, APP

ALIGNMENTS

RESULT 1
US-11-054-515-1881
 Sequence 1881, Application US/11054515
 ; Publication No. US2005025532A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; CURRENT APPLICATION NUMBER: US/11/054,515
 ; FILE REFERENCE: PF52:BP3
 ; CURRENT FILING DATE: 2005-02-10
 ; PRIORITY APPLICATION NUMBER: 60/543,296
 ; PRIORITY FILING DATE: 2004-07-11
 ; PRIORITY APPLICATION NUMBER: 60/580,347
 ; PRIORITY FILING DATE: 2004-06-18
 ; PRIORITY APPLICATION NUMBER: 10/293,418
 ; PRIORITY FILING DATE: 2001-11-14
 ; PRIORITY APPLICATION NUMBER: 60/331,469
 ; PRIORITY FILING DATE: 2001-11-16
 ; PRIORITY APPLICATION NUMBER: 60/340,817
 ; PRIORITY FILING DATE: 2001-12-19
 ; PRIORITY APPLICATION NUMBER: 09/880,748
 ; PRIORITY FILING DATE: 2001-06-15
 ; PRIORITY APPLICATION NUMBER: 60/253,499
 ; PRIORITY FILING DATE: 2001-05-25
 ; PRIORITY APPLICATION NUMBER: 60/277,379
 ; PRIORITY FILING DATE: 2001-03-21
 ; PRIORITY APPLICATION NUMBER: 60/276,248
 ; PRIORITY FILING DATE: 2001-03-16
 ; PRIORITY APPLICATION NUMBER: 60/240,816
 ; PRIORITY FILING DATE: 2000-10-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NO: 3247
 ; SEQ ID NO 1881
 ; LENGTH: 244;
 ; Best Local Similarity 90.1%; Pred. No. 1.7e-32;
 ; Mismatches 2; Indels 0; Gaps 0;
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRQLWNYQQKPEKAPSLIYASSLQGVPS 60
Db 137 DIVMTQSPSTLSASVGDRVTITCRASQISWLYQQKPEKAPKLIIYANSSLQGVPS 196
Qy 61 RFGSGSGTDFLTISGLOPEDATYYCQQTNSYPTFQGTKVIEK 107

Db 197 RFSGSGSGTDFLTISLQQPEDFATYQQANSPLTFGGTKEIK 243
RESULT 2
 US-11-144-248-52
 Sequence 52, Application US/11144248
 Publication No. US20050244408A1
 GENERAL INFORMATION:
 APPLICANT: Cohen, Bruce D.
 APPLICANT: Beebe, Jean
 APPLICANT: Miller, Penelope E.
 APPLICANT: Moyer, James D.
 APPLICANT: Corvalan, Jose R.
 APPLICANT: Gallo, Michael
 TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR 1 RECEPTOR
 FILE REFERENCE: ABX-PFT2
 CURRENT APPLICATION NUMBER: US/11/144,248
 CURRENT FILING DATE: 2005-06-02
 PRIOR APPLICATION NUMBER: US/10/038,591
 PRIOR FILING DATE: 2002-01-04
 PRIOR APPLICATION NUMBER: 60/259,927
 PRIOR FILING DATE: 2001-01-05
 NUMBER OF SEQ ID NOS: 60
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 52
 LENGTH: 236
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-144-248-52

Query Match 87.3%; Score 486; DB 7; Length 236;
 Best Local Similarity 89.7%; Pred. No. 8.2e-32;
 Matches 96; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSAVGDRVTITCRASQISRMWYQQKPEAKSLIYASSLQSGVPS 60
 Db 23 DIQMTQSPSSLSAVGDRVTITCRASQIRNDLGWYQQKPKAPRLLIYASSLQSGVPS 82
 Qy 61 RFSGSGSGTDFLTISLQQPEDFATYQQANSPLTFGGTKEIK 107
 Db 83 RFSGSGSGTDFLTISLQQPEDFATYCLQHNSYPWTIGQSTKVEIK 129

RESULT 3
 US-11-084-554-126
 Sequence 126, Application US/11084554
 GENERAL INFORMATION:
 APPLICANT: Kellermann, Sirid-Ai
 APPLICANT: Korver, Wouter
 APPLICANT: Green, Larry L.
 TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
 FILE REFERENCE: AGENIX 100A
 CURRENT APPLICATION NUMBER: US/11/084,554
 CURRENT FILING DATE: 2005-03-17
 PRIOR APPLICATION NUMBER: 60/554,372
 PRIOR FILING DATE: 2004-03-19
 NUMBER OF SEQ ID NOS: 266
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 126
 LENGTH: 95
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-084-554-126

Query Match 86.9%; Score 484; DB 7; Length 95;
 Best Local Similarity 97.9%; Pred. No. 5.5e-32;
 Matches 93; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 DIQMTQSPSSLSAVGDRVTITCRASQISRMWYQQKPEAKSLIYASSLQSGVPS 60
 Qy 61 RFSGSGSGTDFLTISLQQPEDFATYQQANSPLTFGGTKEIK 107
 Db 61 RFSGSGSGTDFLTISLQQPEDFATYQQANSPLTFGGTKEIK 107
 Qy 61 RFSGSGSGTDFLTISLQQPEDFATYQQANSPLTFGGTKEIK 107
 Db 61 RFSGSGSGTDFLTISLQQPEDFATYQQANSPLTFGGTKEIK 107

RESULT 4
 US-11-084-554-1
 Sequence 1, Application US/11084554
 Publication No. US20050260679A1
 GENERAL INFORMATION:
 APPLICANT: Kellermann, Sirid-Ai
 APPLICANT: Korver, Wouter
 APPLICANT: Green, Larry L.
 TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
 FILE REFERENCE: AGENIX 100A
 CURRENT APPLICATION NUMBER: US/11/084,554
 CURRENT FILING DATE: 2005-03-17
 PRIOR APPLICATION NUMBER: 60/554,372
 PRIOR FILING DATE: 2004-03-19
 NUMBER OF SEQ ID NOS: 266
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 1
 LENGTH: 107
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-084-554-1

Query Match 86.9%; Score 484; DB 7; Length 107;
 Best Local Similarity 88.8%; Pred. No. 6e-32;
 Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSAVGDRVTITCRASQISRMWYQQKPEAKSLIYASSLQSGVPS 60
 Db 1 DIQMTQSPSSLSAVGDRVTITCRASQGRNLYQQKPKAPRLLIYASSLQSGVPS 60
 Qy 61 RFSGSGSGTDFLTISLQQPEDFATYQQANSPLTFGGTKEIK 107
 Db 61 RFSGSGSGTDFLTISLQQPEDFATYQQANSPLTFGGTKEIK 107

RESULT 5
 US-11-144-248-48
 Sequence 48, Application US/11144248
 Publication No. US20050244408A1
 GENERAL INFORMATION:
 APPLICANT: Cohen, Bruce D.
 APPLICANT: Beebe, Jean
 APPLICANT: Miller, Penelope B.
 APPLICANT: Moyer, James D.
 APPLICANT: Corvalan, Jose R.
 APPLICANT: Gallo, Michael
 TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR 1 RECEPTOR
 FILE REFERENCE: ABX-PF2
 CURRENT APPLICATION NUMBER: US/11/144,248
 CURRENT FILING DATE: 2005-06-02
 PRIOR APPLICATION NUMBER: US/10/038,591
 PRIOR FILING DATE: 2002-01-04
 PRIOR APPLICATION NUMBER: 60/259,927
 PRIOR FILING DATE: 2001-01-05
 NUMBER OF SEQ ID NOS: 60
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 48
 LENGTH: 236
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-144-248-48

Query Match 86.9%; Score 484; DB 7; Length 95;
 Best Local Similarity 97.9%; Pred. No. 5.5e-32;
 Matches 93; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 86.9%; Score 484; DB 7; Length 236;
 Best Local Similarity 88.8%; Pred. No. 1.2e-31;
 Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTQSSSLASVGDEVTITCRASQISRMALWYQQKPEKAPSKLIYASSLQGVPS 60
 Db 23 DIQMTQSSSLASVGDEVTITCRASQISRMALWYQQKPEKAPSKLIYASSLQGVPS 82

Qy 61 RFSGSGSGTDFLTISGLQPEDATYYCQQINSYPRFGQGTKEIK 107
 Db 83 RFSGSGSGTDFLTISGLQPEDATYYCQLQNSYPTFGQGTKEIK 129

RESULT 6
US-11-054-515-82

Sequence 82, Application US/11/054515
 Publication No. US2005025532A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 FILE REFERENCE: PFP23P3
 CURRENT APPLICATION NUMBER: US/11/054,515
 PRIOR APPLICATION NUMBER: 2005-02-10
 PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: 60/543,296
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 10/293,418
 PRIOR FILING DATE: 2002-11-14
 PRIOR APPLICATION NUMBER: 60/331,469
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/340,817
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 09/880,748
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: 60/293,499
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/277,379
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/340,816
 PRIOR FILING DATE: 2000-10-17
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 3247

RESULT 8
US-11-054-669-62
 Sequence 62, Application US/11/054669
 Publication No. US20050261180A1
 GENERAL INFORMATION:
 APPLICANT: Foote, Jefferson
 TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
 FILE REFERENCE: 3019/US/3
 CURRENT APPLICATION NUMBER: US/11/054,669
 CURRENT FILING DATE: 2005-02-08
 PRIOR APPLICATION NUMBER: US 10/194,975
 PRIOR FILING DATE: 2002-07-12
 PRIOR APPLICATION NUMBER: US 60/305,111
 PRIOR FILING DATE: 2001-07-12
 NUMBER OF SEQ ID NOS: 124
 SEQ ID NO 62
 LENGTH: 244
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-054-515-82

Query Match 86.7%; Score 483; DB 7; Length 244;
 Best Local Similarity 87.9%; Pred. No. 1.4e-31;
 Matches 94; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTQSSSLASVGDEVTITCRASQISRMALWYQQKPEKAPSKLIYASSLQGVPS 60
 Db 137 DIQMTQSSSLASVGDEVTITCRASQISRMALWYQQKPEKAPSKLIYASSLQGVPS 196

Qy 61 RFSGSGSGTDFLTISGLQPEDATYYCQQINSYPRFGQGTKEIK 107
 Db 157 RFSGSGSGTDFLTISGLQPEDATYYCQKNSAPYFGQGTKEIK 243

RESULT 7
US-11-054-515-261

Sequence 261, Application US/11/054515
 Publication No. US2005025532A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 FILE REFERENCE: PFP23P3
 CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT FILING DATE: 2005-02-10
 PRIOR APPLICATION NUMBER: 60/543,296
 PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: 60/580,347
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 60/331,418
 PRIOR FILING DATE: 2002-11-14
 PRIOR APPLICATION NUMBER: 60/293,418
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/331,469
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/277,379
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/340,816
 PRIOR FILING DATE: 2000-10-17
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 3247

Query Match 86.0%; Score 479; DB 7; Length 95;
 Best Local Similarity 96.8%; Pred. No. 1.3e-31;
 Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLASVGDRVTITCRASQISRMALWYQQKPEKAPSKLIYASSLQGVPS 60
 Db 1 DIQMTQSPSSLASVGDRVTITCRASQISRMALWYQQKPEKAPSKLIYASSLQGVPS 60

Qy 61 RFSGSGSGTDFLTISGLQPEDATYYCQQINSYPRFGQGTKEIK 107
 Db 157 RFSGSGSGTDFLTISGLQPEDATYYCQKNSAPYFGQGTKEIK 243

Query Match 86.7%; Score 483; DB 7; Length 244;
 Best Local Similarity 87.9%; Pred. No. 1.4e-31;
 Matches 94; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLASVGDRVTITCRASQISRMALWYQQKPEKAPSKLIYASSLQGVPS 60
 Db 1 DIQMTQSPSSLASVGDRVTITCRASQISRMALWYQQKPEKAPSKLIYASSLQGVPS 60

Qy 61 RFSGSGSGTDFLTISGLQPEDATYYCQQINSYPRFGQGTKEIK 107
 Db 157 RFSGSGSGTDFLTISGLQPEDATYYCQKNSAPYFGQGTKEIK 243

RESULT 9

US-11-096-074-53
 Sequence 53, Application US/11096074
 PUBLICATION NO. US20050260193A1
 GENERAL INFORMATION:
 APPLICANT: LIEBERBURG, IVAN
 TITLE OF INVENTION: STEROID SPARING AGENTS AND METHODS OF USING SAME
 FILE REFERENCE: 034008-112
 CURRENT APPLICATION NUMBER: US/11/096, 074
 CURRENT FILING DATE: 2005-04-01
 PRIOR APPLICATION NUMBER: 60/558, 120
 PRIOR FILING DATE: 2004-04-01
 NUMBER OF SEQ ID NOS: 60
 SOFTWARE: PatentIn Ver. 3.3
 SEQ ID NO 53
 LENGTH: 113
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: MOD RES
 LOCATION: (31) .. (32)
 OTHER INFORMATION: Variable amino acid

US-11-096-074-53

Query Match 86.0%; Score 479; DB 7; Length 244;
 Best Local Similarity 86.9%; Pred. No. 2.9e-31;
 Matches 93; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
 SEQ ID NO 164
 LENGTH: 244
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-054-515-164

Query Match 86.0%; Score 479; DB 7; Length 244;
 Best Local Similarity 86.9%; Pred. No. 2.9e-31;
 Matches 93; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSAVGDRVTITRASQTSRILAWYQKPEKAPSLIYAASSLQSGVPS 60
 Db 137 DIQMTQSPSSLSAVGDRVTITRASQGIRNYLAWQKPGKAPKLLIYAASTLQSGVPS 196

Qy 61 RFGSGSGSGTDFLTISLQPEDFATYYCQQNSYPRTEFGQGTKEIK 107
 Db 197 RFGSGSGSGTDFLTISLQPEDFATYYCQQNSYPRTEFGQGTKEIK 243

RESULT 11

US-11-054-515-280
 Sequence 280, Application US/11054515
 Publication No. US2005025532A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 FILE REFERENCE: PF523P3
 CURRENT APPLICATION NUMBER: US/11/054, 515
 CURRENT FILING DATE: 2005-02-10
 PRIOR APPLICATION NUMBER: 60/543, 296
 PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: 60/580, 347
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 10/293, 418
 PRIOR FILING DATE: 2002-11-14
 PRIOR APPLICATION NUMBER: 60/331, 469
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/340, 817
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 09/880, 748
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: 60/293, 499
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/277, 379
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/276, 248
 PRIOR FILING DATE: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/240, 816
 PRIOR FILING DATE: 2000-10-17
 Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 3247

SEQ ID NO 280
 LENGTH: 244
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-054-515-280

Query Match 85.8%; Score 478; DB 7; Length 244;
 Best Local Similarity 86.9%; Pred. No. 3.5e-31;
 Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSAVGDRVTITRASQTSRILAWYQKPEKAPSLIYAASSLQSGVPS 60
 Db 137 DIQMTQSPSSLSAVGDRVTITRASQGIRNYLAWQKPGKAPKLLIYAASTLQSGVPS 196

Qy 61 RFGSGSGSGTDFLTISLQPEDFATYYCQQNSYPRTEFGQGTKEIK 107
 Db 197 RFGSGSGSGTDFLTISLQPEDFATYYCQQNSYPRTEFGQGTKEIK 243

RESULT 12

US-11-054-515-1882
 Sequence 1882, Application US/11054515
 Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 3247

Publication No. US20050255532A1
 GENERAL INFORMATION:
 / APPLICANT: Ruben et al.
 / TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 FILE REFERENCE: PFS23P3
 CURRENT APPLICATION NUMBER: US/11/054,515
 CURRENT FILING DATE: 2005-02-10
 PRIOR APPLICATION NUMBER: 60/543,296
 PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: 60/580,347
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 10/293,418
 PRIOR APPLICATION NUMBER: 60/331,469
 PRIOR FILING DATE: 2002-11-14
 PRIOR APPLICATION NUMBER: 60/340,817
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 09/880,748
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: 60/293,499
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/277,379
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/276,248
 PRIOR FILING DATE: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/240,816
 PRIOR FILING DATE: 2000-10-17
 Remaining Prior Application data removed - See File Wrapper or PALM.
 SEQ ID NO: 1882
 LENGTH: 239
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-054-515-1882

Query Match 85.6%; Score 477; DB 7; Length 239;
 Best Local Similarity 84.1%; Pred. No. 4.1e-31;
 Matches 90; Conservative 7; Mismatches 10; Indels 0;
 Gaps 0;

Qy 1 DIQMTOQSPSSLISASVGDRVTITCRASGIGKPKPEAKSLLIYASSLQSGVPS 60
 Db 132 DIQMTOQSPSTISASIGDRVTITCRASGIGKPKPEAKSLLIYASSLQSGVPS 60
 Qy 61 RFSGSGSGTDFLTISGLQPEDFATYYCQQNSYPRTFGGTKVEIK 107
 Db 192 RFSGSGSGTDFLTSSLQDDFATYYCQQNSYPLTFGGTKLEIK 238

RESULT 14
 US-11-054-515-1889
 / Sequence 1889, Application US/11/054515
 / Publication No. US20050255532A1
 / GENERAL INFORMATION:
 / APPLICANT: Ruben et al.
 / TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 FILE REFERENCE: PFS23P3
 CURRENT APPLICATION NUMBER: US/11/054,515
 CURRENT FILING DATE: 2005-02-10
 PRIOR APPLICATION NUMBER: 60/543,296
 PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: 60/580,347
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 10/293,418
 PRIOR FILING DATE: 2002-11-14
 PRIOR APPLICATION NUMBER: 60/331,469
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/340,817
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 09/880,748
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: 60/277,379
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/276,248
 PRIOR FILING DATE: 2001-03-16
 PRIOR FILING DATE: 2000-10-17
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 3247
 SEQ ID NO: 1889
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-054-515-1889

Query Match 85.6%; Score 477; DB 7; Length 241;
 Best Local Similarity 84.1%; Pred. No. 4.1e-31;
 Matches 90; Conservative 7; Mismatches 10; Indels 0;
 Gaps 0;

Qy 1 DIQMTOQSPSSLISASVGDRVTITCRASGIGKPKPEAKSLLIYASSLQSGVPS 60
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 Qy 61 RFSGSGSGTDFLTISGLQPEDFATYYCQQNSYPRTFGGTKVEIK 107

Db 194 RFSGSGSGTDFLTISLQDDFATYYCQQYSNPLTFCGGTKLEIK 240

RESULT 15
US-11-054-515-1901

/ Sequence 1901, Application US/11054515

/ Publication No. US20050255532A1

/ GENERAL INFORMATION:

/ APPLICANT: Ruben et al.

/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

/ FILE REFERENCE: PFS2AP3

/ CURRENT APPLICATION NUMBER: US/11/054,515

/ PRIOR APPLICATION NUMBER: 60/531,296

/ PRIOR FILING DATE: 2004-02-10

/ PRIOR APPLICATION NUMBER: 60/580,347

/ PRIOR FILING DATE: 2004-06-18

/ PRIOR APPLICATION NUMBER: 10/293,418

/ PRIOR FILING DATE: 2002-11-14

/ PRIOR APPLICATION NUMBER: 60/331,469

/ PRIOR FILING DATE: 2001-11-16

/ PRIOR APPLICATION NUMBER: 60/340,817

/ PRIOR FILING DATE: 2001-12-19

/ PRIOR APPLICATION NUMBER: 09/880,748

/ PRIOR FILING DATE: 2001-06-15

/ PRIOR APPLICATION NUMBER: 60/293,499

/ PRIOR FILING DATE: 2001-05-25

/ PRIOR APPLICATION NUMBER: 60/277,379

/ PRIOR FILING DATE: 2001-03-21

/ PRIOR APPLICATION NUMBER: 60/276,248

/ PRIOR FILING DATE: 2001-03-16

/ PRIOR APPLICATION NUMBER: 60/240,816

/ PRIOR FILING DATE: 2000-10-17

/ Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247

SEQ ID NO 1901

/ LENGTH: 241

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-11-054-515-1901

Query Match 85.6%; Score 477; DB 7; Length 241;
Best Local Similarity 84.1%; Pred. No. 4.1e-31;
Matches 90; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

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Db 134 DIQMTQSPLSASGDRVTITCRASEGITHWLWYQQPKBPKPSLIYKASSLASGAFS 193

Qy 61 RFSGSGSGTDFLTISLQDDFATYYCQQYSNPLTFCGGTKLEIK 107

Db 194 RFSGSGSGTDFLTISLQDDFATYYCQQYSNPLTFCGGTKLEIK 240

Search completed: December 3, 2005, 14:17:54
Job time : 6.11429 sec

Run on:	December 3, 2005, 14:11:48	Search time 188.669 Seconds (without alignments)
Title:	US-10-769-144-8	
Perfect score:	557	
Sequence:	1 NTOWWNEPSSSTCSAISYRQDYM	COOIVSYDPMGCGCCTKQETIK 107
Om protein - protein search, using Bw model		
Copyright (c) 1993 - 2005 Compugen Ltd.		
P01594 homo sapien		KV1B_HUMAN
P01602 homo sapien		KV1J_HUMAN
P01603 homo sapien		KV1K_HUMAN
P80362 homo sapien		KV1Y_HUMAN
Osef6 homo sapien		QSBEF6_HUMAN
P01608 homo sapien		KV1P_HUMAN
P01606 homo sapien		KV1N_HUMAN
P01609 homo sapien		KV1Q_HUMAN
P01595 homo sapien		KV1C_HUMAN
P01697 homo sapien		Q56917_HUMAN
P04432 homo sapien		KV1X_HUMAN
P01613 homo sapien		KV1U_HUMAN
P01643 mus musculus		KV1F_HUMAN
O96PF6_HITMAN		

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5									
Searched: 2166443 seqs, 70528306 residues									
Total number of hits satisfying chosen parameters: 2166443									
Minimum DB seq length: 0									
Maximum DB seq length: 2000000000									
Post-processing: Minimum Match 0% Maximum Match 100%									
Database : UniProt_05-80: 1: uniprot_sprot: 2: uniprot_trembl: * Listing first 45 summaries									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description				
1	508	91.2	236	2	Q6GMX9_HUMAN	Q6gmx9 homo sapien			
2	494	88.7	108	2	Q9UL70_HUMAN	Q9ul70 homo sapien			
3	494	88.7	236	2	Q6GMX8_HUMAN	Q6gmx8 homo sapien			
4	492	88.3	236	2	Q502W4_HUMAN	Q502w4 homo sapien			
5	481	86.4	236	2	Q7Z3Y4_HUMAN	Q7z3y4 homo sapien			
6	479	86.0	117	1	KV11_HUMAN	KV11_HUMAN			
7	477	85.6	244	2	Q652C8_HUMAN	Q652c8 homo sapien			
8	476	85.5	108	1	KV1G_HUMAN	KV1G_HUMAN			
9	474	85.1	108	1	KV1V_HUMAN	KV1V_HUMAN			
10	474	85.1	240	2	Q652C9_HUMAN	Q652c9 homo sapien			
11	472	84.7	236	2	Q6GMW1_HUMAN	Q6gmw1 homo sapien			
12	471	84.6	236	2	Q6PIH7_HUMAN	Q6pih7 homo sapien			
13	468	84.0	108	1	KV1F_HUMAN	KV1F_HUMAN			
14	467	83.8	108	1	KV1L_HUMAN	KV1L_HUMAN			
15	465	83.5	108	1	KV1R_HUMAN	KV1R_HUMAN			
16	461	82.8	108	1	Q9UL77_HUMAN	Q9ul77 homo sapien			
17	460	82.6	108	2	Q9UL79_HUMAN	Q9ul79 homo sapien			
18	460	82.6	236	2	Q6P1H4_HUMAN	Q6p1h4 homo sapien			
19	459	82.4	108	1	KV1M_HUMAN	KV1M_HUMAN			
20	457	82.1	107	1	KV1D_HUMAN	KV1D_HUMAN			
21	456	81.9	108	1	KV1A_HUMAN	KV1A_HUMAN			
22	456	81.9	236	2	Q6P1T5_HUMAN	Q6p1t5 homo sapien			
23	455	81.8	107	2	Q96SA9_HUMAN	Q96sa9 homo sapien			
24	453	81.3	108	1	KV1S_HUMAN	KV1S_HUMAN			
25	448	80.4	234	2	Q7Z4T3_HUMAN	Q7z4t3 homo sapien			
26	447	80.3	108	1	KV1M_HUMAN	KV1M_HUMAN			
27	446	80.1	129	1	KV1W_HUMAN	KV1W_HUMAN			
28	444	79.8	107	2	Q9UL81_HUMAN	Q9ul81 homo sapien			
29	443	79.5	108	1	KV1E_HUMAN	KV1E_HUMAN			
30	443	79.5	236	2	Q6GMXO_HUMAN	Q6gmxo homo sapien			
31	441	79.2	108	1	KV1O_HUMAN	KV1O_HUMAN			

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ID Q502W4;								
AC Q502W4;								
DT 13-SEP-2005 (TREMBLrel. 31; Created)								
DT 13-SEP-2005 (TREMBLrel. 31; Last sequence update)								
DT 13-SEP-2005 (TREMBLrel. 31; Last annotation update)								
DE IGKC Protein.								
NAME IgKC;								
OS Homo sapiens (Human);								
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.								
OC NCBI_TaxID=9606;								
OX NCBI_TaxID=9606;								
RN [1]								
RP NUCLEOTIDE SEQUENCE.								
RC TISSUE=Glandular pool- thyroid.								
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1101/0793/pnas.242603899;								
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schueler G.D., Altshuler S.P., Zeeberg B., Bustow K.H., Schaefer C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heihs F., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Logquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., FAHHEY J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).								
RL RN [2]								
RP NUCLEOTIDE SEQUENCE.								
RC TISSUE=Skeletal Muscle;								
RA Strausberg R.L.; Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.								
RX EMBL; BC095489; AAH05332.1; -; mRNA.								
DR HSSP; P01834; IHEZ.								
DR Ensembl; ENSG00000163245; Homo sapiens.								
DR InterPro; IPR003006; Ig_MHC.								
DR InterPro; IPR007110; Ig_C1.								
DR InterPro; IPR003597; Ig_V.								
DR SMART; SM00406; Cl-Bet_1.								
DR PROSITE; PS50035; Ig_LIKE; 2.								
DR PROSITE; PS00290; Ig_MHC; UNKNOWN_1.								
KW Hypothetical protein; Immunoglobulin domain.								
DR Best Local Similarity 87.9%; Pred. No. 1e-39; Matches 94; Conservative 94; MisMatches 4; Indels 0; Gaps 0;								
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DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
DR Sequence 236 AA; Score 492; DB 2; Length 236;								
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DR SMART; SM00406; Ig_V.								
DR PROSITE; PS50035; Ig_LIKE; 2.								
DR SMART; SM00407; Ig_C1; 1.								
DR SMART; SM00406; Ig_V.								
DR PROSITE; PS00290; Ig_MHC; UNKNOWN_1.								
DR Sequence 25936 MW; E2DP79AC18756AR9 CRC64;								
DR Query Match 88.3%; Score 492; DB 2; Length 236;								
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DR Sequence 25936 MW; E2DP79AC18756AR9 CRC64;								
DR Query Match 64 KF11_HUMAN STANDARD;								
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DR Sequence 25936 MW; E2DP79AC18756AR9 CRC64;								
DR Query Match 65 KF11_HUMAN STANDARD;								
DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
DR Sequence 25936 MW; E2DP79AC18756AR9 CRC64;								
DR Query Match 66 KF11_HUMAN STANDARD;								
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DR Sequence 25936 MW; E2DP79AC18756AR9 CRC64;								
DR Query Match 67 KF11_HUMAN STANDARD;								
DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
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DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
DR Sequence 25936 MW; E2DP79AC18756AR9 CRC64;								
DR Query Match 69 KF11_HUMAN STANDARD;								
DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
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DR Query Match 70 KF11_HUMAN STANDARD;								
DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
DR Sequence 25936 MW; E2DP79AC18756AR9 CRC64;								
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DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
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DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
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DR Query Match 78 KF11_HUMAN STANDARD;								
DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
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DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
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DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
DR Sequence 25936 MW; E2DP79AC18756AR9 CRC64;								
DR Query Match 81 KF11_HUMAN STANDARD;								
DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
DR Sequence 25936 MW; E2DP79AC18756AR9 CRC64;								
DR Query Match 82 KF11_HUMAN STANDARD;								
DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
DR Sequence 25936 MW; E2DP79AC18756AR9 CRC64;								
DR Query Match 83 KF11_HUMAN STANDARD;								
DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
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DR Query Match 84 KF11_HUMAN STANDARD;								
DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
DR Sequence 25936 MW; E2DP79AC18756AR9 CRC64;								
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DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
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DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
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DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
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DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
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DR Query Match 91 KF11_HUMAN STANDARD;								
DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
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DR Query Match 92 KF11_HUMAN STANDARD;								
DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
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DR Query Match 93 KF11_HUMAN STANDARD;								
DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
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DR Query Match 94 KF11_HUMAN STANDARD;								
DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
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DR Query Match 95 KF11_HUMAN STANDARD;								
DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								
DR Sequence 25936 MW; E2DP79AC18756AR9 CRC64;								
DR Query Match 96 KF11_HUMAN STANDARD;								
DR Best Local Similarity 89.7%; Pred. No. 8.2e-41; Matches 3; MisMatches 8; Indels 0; Gaps 0;								

page 4

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE TrEMBLrel. 27, Last annotation update)
 IGKC protein.
 GN Name=IGKC;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RX MEDLINE=2388857; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Colling F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Altschul S.F., Zeisberg B., Buetow K.H., Schaefer C.F., Blat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marsuska K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Bonaldo M.P., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahay S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hale S.W.,
 RA Villalon D.K., Murzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Paney J., Heiton B., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shvchenko Y., Boutjard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RG NIH MGC Project;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
 EMBL; BC073791; AAH73791.1; -; mRNA.
 DR SMR; Q6GPW1; 24-236.
 DR Ensembl; ENSG00000163245; Homo sapiens.
 InterPro; IPR003599; Ig.
 InterPro; IPR07110; Ig-like.
 InterPro; IPR003597; Ig_C1.
 InterPro; IPR003036; Ig_MHC.
 InterPro; IPR003598; Ig_v.
 DR Pfam; PF07654; Cl-set; 1.
 SMART; SM000409; Ig_2.
 SMART; SM000407; IgC1; 1.
 SMART; SM000406; IgV; 1.
 PROSITE; PS50835; Ig_LIKE; 2.
 PROSITE; PS00290; Ig_MHC; UNKNOWN 1.
 SEQUENCE 236 AA; 25751 MW; SBEFE6AA087AFAC437 CRC64;

Query Match 84.7%; Score 472; DB 2; Length 236;
 Best Local Similarity 89.6%; Pred. No. 8-1e-39;
 Matches 95; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
 Gaps 0; Gaps 0;

Qy 2 IQMTOQSPSLSASVGDRVTITCRASQGIGRRLWYQQKEDEKAPKSLIYASSLQSQVPSR 61
 Db 24 IQMTOQSPSLSASVGDRVTITCRASQGIGRRLWYQQKEDEKAPKSLIYASSLQSQVPSR 83

Qy 62 FSGGGSGTGTDTLTISGLOPDEDATYYCOQYNSYPRTFGCGTQVKEIK 107
 Db 84 FSGGGSGTGTDTLTISLQPEDATYYCLODNYDWTFGGTQVKEIK 129

Query Match 84.6%; Score 471; DB 2; Length 236;
 Best Local Similarity 86.9%; Pred. No. 1e-38;
 Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIOQTOQSPSLSASVGDRVTITCRASQGIGRRLWYQQKEDEKAPKSLIYASSLQSQVPS 60
 Db 23 DIQTOQSPSLSASVGDRVTITCRASQGIGRRLWYQQKEDEKAPKSLIYASSLQSQVPS 82

Qy 61 RFSGGGSGTGTDTLTISGLOPDEDATYYCOQYNSYPRTFGCGTQVKEIK 107
 Db 83 RFSGGGSGTGTDTLTISLQPEDATYYCLODNYDWTFGGTQVKEIK 129

RESULT 13

KV1F HUMAN
 ID KV1F_HUMAN STANDARD;
 AC P01598;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

RC TISSUE=lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Colling F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Altschul S.F., Zeisberg B., Buetow K.H., Schaefer C.F., Blat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marsuska K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Bonaldo M.P., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahay S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hale S.W.,
 RA Villalon D.K., Murzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Paney J., Heiton B., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shvchenko Y., Boutjard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 NUCLEOTIDE SEQUENCE.
 RC TISSUE=lung;
 RG NIH MGC Project;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
 EMBL; BC034141; AAH34141.1; -; mRNA.
 DR HSSP; P01607; 1AR2.
 DR SMR; Q6PHH7; 23-236.
 DR Ensembl; ENSG00000163245; Homo sapiens.
 InterPro; IPR003599; Ig.
 InterPro; IPR07110; Ig-like.
 InterPro; IPR003597; Ig_C1.
 InterPro; IPR003036; Ig_MHC.
 InterPro; IPR003598; Ig_v.
 DR Pfam; PF07654; Cl-set; 1.
 SMART; SM000409; Ig_2.
 SMART; SM000407; IgC1; 1.
 SMART; SM000406; IgV; 1.
 PROSITE; PS50835; Ig_LIKE; 2.
 PROSITE; PS00290; Ig_MHC; UNKNOWN 1.
 SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

DT	10-MAY-2005	(Rel. 47, Last annotation update)
Ig kappa chain V-I region EU.		
Homo sapiens (Human).		
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
NCBI_TAXID=9606;		
[1]	RN	RN
PROTEIN SEQUENCE;	PUBMED=5489770;	PROTEIN SEQUENCE;
MEDLINE=71064023;	PUBMED=112021;	MEDLINE=79237922;
Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.; "The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";	PubMed=112021;	PubMed=112021;
Biochemistry 9:3155-3161(1970).		
[2]	RN	RN
DISULFIDE BOND;	MEDLINE=71064027;	MEDLINE=71064027;
Gall W.E., Edelman G.M.; "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";	PubMed=4923144;	PubMed=4923144;
Biochemistry 9:3188-3196(1970).		
-1 - MISCELLANEOUS:	The C region of this chain has the INV (3) marker.	
-1 - MISCELLANEOUS:	This chain was isolated from a myeloma protein.	
CC	CC	CC
PIR; A90562; KIHUEU.		
DR HSSP; P01607; IBWW.		
SMR; P01598; 1_107.		
Ensembl; BNSG00000163245; Homo sapiens.		
GO; GO:000576: C: extracellular region; NAS.		
GO; GO:0003823; F: antigen binding; NAS.		
InterPro; IPR007110; Ig-like.		
InterPro; IPR003596; Ig_v.		
SMART; SM00406; Ig_LIKE_1.		
PROSITE; PS50835; Ig_LIKE_1.		
Bence-Jones Protein; Direct protein sequencing; Immunoglobulin domain.		
KW Immunoglobulin V region.		
FT REGION 1 23 Framework-1.		Framework-1.
FT REGION 24 34 Framework-2.		Framework-2.
FT REGION 35 49 Framework-3.		Framework-3.
FT REGION 50 56 Framework-4.		Framework-4.
FT REGION 57 88 Complementarity-determining-1.		Complementarity-determining-1.
FT REGION 89 97 Complementarity-determining-2.		Complementarity-determining-2.
FT REGION 98 107 Complementarity-determining-3.		Complementarity-determining-3.
FT DISULFID 23 88 Complementarity-determining-4.		Complementarity-determining-4.
NON TER 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;		
SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90E4E98 CRC64;		
Query Match 84.0%; Score 468; DB 1; Length 108;		
Best Local Similarity 83.2%; Pred. No. 8 4e-39;		
Matches 89; Conservative 8; Mismatches 10; Indels 0; Gaps 0;		
Db	Db	Db
RESULT 15		
KV1_HUMAN STANDARD; PRT; 108 AA.		
ID KV1_HUMAN STANDARD; PRT; 108 AA.		
AC P01610;		
DT 21-JUL-1986 (Rel. 01, Created)		
DT 21-JUL-1986 (Rel. 01, Last sequence update)		
DT 10-MAY-2005 (Rel. 47, Last annotation update)		
DE 19 kappa chain V-I region WEA.		
OS Homo sapiens (Human)		
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC Homo.		
NCBI_TAXID=9606;		
[1]	RN	RN
PROTEIN SEQUENCE;	PUBMED=5489770;	PROTEIN SEQUENCE;
MEDLINE=71064023;	PubMed=112021;	MEDLINE=79237922;
Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.; "The primary structure of the Bence-Jones protein Rue. The amino acid sequence of the variable part of a human L-chain of the kappa-type.";	PubMed=112021;	PubMed=112021;
Hoppe-Seyler's Z. Physiol. Chem. 360:734(1979).		
-1 - MISCELLANEOUS: This is a Bence-Jones protein.		
CC	CC	CC
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CC	CC	CC
DR PIR; A01870; KIHUEU.		
DR HSSP; P01607; IBWW.		
SMR; P01604; 1_108.		
GO; GO:0005576; C: extracellular region; NAS.		
GO; GO:0003823; F: antigen binding; NAS.		
GO; GO:0006955; P: immune response; NAS.		
InterPro; IPR007110; Ig-like.		
InterPro; IPR003596; Ig_v.		
SMART; SM00406; Ig_LIKE_1.		
PROSITE; PS50835; Ig_LIKE_1.		
Bence-Jones Protein; Direct protein sequencing; Immunoglobulin domain.		
KW Immunoglobulin V region.		
FT REGION 1 23 Framework-1.		Framework-1.
FT REGION 24 34 Framework-2.		Framework-2.
FT REGION 35 49 Framework-3.		Framework-3.
FT REGION 50 56 Framework-4.		Framework-4.
FT REGION 57 88 Complementarity-determining-1.		Complementarity-determining-1.
FT REGION 89 97 Complementarity-determining-2.		Complementarity-determining-2.
FT REGION 98 107 Complementarity-determining-3.		Complementarity-determining-3.
FT DISULFID 23 88 Complementarity-determining-4.		Complementarity-determining-4.
NON TER 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;		
SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90E4E98 CRC64;		
Query Match 83.8%; Score 467; DB 1; Length 108;		
Best Local Similarity 81.3%; Pred. No. 1_1e-36;		
Matches 87; Conservative 9; Mismatches 9; Indels 0; Gaps 0.		
Qy	Qy	Qy
1 DIQMTOSSSILASAVGDRVTITCRASQISRMLAWYQQKPEKAKSLIYAASSLQSGVPS 60		
1 DIQMTOSSSILASAVGDRVTITCRASQISRMLAWYQQKPEKAKSLIYAASSLQSGVPS 60		
61 RFGSGSGTDFLTISQLQPEDPATYCQINSYPRTFGGTKVEIK 107		
61 RFGSGSGTDFLTISQLQPEDPATYCQINSYPRTFGGTKVEIK 107		
61 RFGSGSGTDFLTISQLQPEDPATYCQINSYPRTFGGTKVEIK 107		
RESULT 14		
KV1_HUMAN STANDARD; PRT; 108 AA.		
ID KV1_HUMAN STANDARD; PRT; 108 AA.		
AC P01604;		
DT 21-JUL-1986 (Rel. 01, Created)		
DT 21-JUL-1986 (Rel. 01, Last sequence update)		
DT 10-MAY-2005 (Rel. 47, Last annotation update)		
DE 19 kappa chain V-I region WEA.		
OS Homo sapiens (Human)		
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC Homo.		
NCBI_TAXID=9606;		
[1]	RN	RN
PROTEIN SEQUENCE;	PUBMED=5489770;	PROTEIN SEQUENCE;
MEDLINE=71064023;	PubMed=112021;	MEDLINE=79237922;
Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.; "The primary structure of the Bence-Jones protein Rue. The amino acid sequence of the variable part of a human L-chain of the kappa-type.";	PubMed=112021;	PubMed=112021;
Hoppe-Seyler's Z. Physiol. Chem. 360:734(1979).		
-1 - MISCELLANEOUS: This is a Bence-Jones protein.		
CC	CC	CC
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CC	CC	CC
DR PIR; A01870; KIHUEU.		
DR HSSP; P01607; IBWW.		
SMR; P01604; 1_108.		
GO; GO:0005576; C: extracellular region; NAS.		
GO; GO:0003823; F: antigen binding; NAS.		
GO; GO:0006955; P: immune response; NAS.		
InterPro; IPR007110; Ig-like.		
InterPro; IPR003596; Ig_v.		
SMART; SM00406; Ig_LIKE_1.		
PROSITE; PS50835; Ig_LIKE_1.		
Bence-Jones Protein; Direct protein sequencing; Immunoglobulin domain.		
KW Immunoglobulin V region.		
FT REGION 1 23 Framework-1.		Framework-1.
FT REGION 24 34 Framework-2.		Framework-2.
FT REGION 35 49 Framework-3.		Framework-3.
FT REGION 50 56 Framework-4.		Framework-4.
FT REGION 57 88 Complementarity-determining-1.		Complementarity-determining-1.
FT REGION 89 97 Complementarity-determining-2.		Complementarity-determining-2.
FT REGION 98 107 Complementarity-determining-3.		Complementarity-determining-3.
FT DISULFID 23 88 Complementarity-determining-4.		Complementarity-determining-4.
NON TER 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;		
SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90E4E98 CRC64;		
Query Match 83.8%; Score 467; DB 1; Length 108;		
Best Local Similarity 83.2%; Pred. No. 8 4e-39;		
Matches 89; Conservative 8; Mismatches 10; Indels 0; Gaps 0;		
Db	Db	Db
RESULT 15		
KV1_HUMAN STANDARD; PRT; 108 AA.		
ID KV1_HUMAN STANDARD; PRT; 108 AA.		
AC P01610;		
DT 21-JUL-1986 (Rel. 01, Created)		
DT 21-JUL-1986 (Rel. 01, Last sequence update)		
DT 10-MAY-2005 (Rel. 47, Last annotation update)		
DE 19 kappa chain V-I region WEA.		
OS Homo sapiens (Human)		
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC Homo.		
NCBI_TAXID=9606;		
[1]	RN	RN
PROTEIN SEQUENCE;	PUBMED=5489770;	PROTEIN SEQUENCE;
MEDLINE=71064023;	PubMed=112021;	MEDLINE=79237922;
Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.; "The primary structure of the Bence-Jones protein Rue. The amino acid sequence of the variable part of a human L-chain of the kappa-type.";	PubMed=112021;	PubMed=112021;
Hoppe-Seyler's Z. Physiol. Chem. 360:734(1979).		
-1 - MISCELLANEOUS: This is a Bence-Jones protein.		
CC	CC	CC
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CC	CC	CC
DR PIR; A01870; KIHUEU.		
DR HSSP; P01607; IBWW.		
SMR; P01604; 1_108.		
GO; GO:0005576; C: extracellular region; NAS.		
GO; GO:0003823; F: antigen binding; NAS.		
GO; GO:0006955; P: immune response; NAS.		
InterPro; IPR007110; Ig-like.		
InterPro; IPR003596; Ig_v.		
SMART; SM00406; Ig_LIKE_1.		
PROSITE; PS50835; Ig_LIKE_1.		
Bence-Jones Protein; Direct protein sequencing; Immunoglobulin domain.		
KW Immunoglobulin V region.		
FT REGION 1 23 Framework-1.		Framework-1.
FT REGION 24 34 Framework-2.		Framework-2.
FT REGION 35 49 Framework-3.		Framework-3.
FT REGION 50 56 Framework-4.		Framework-4.
FT REGION 57 88 Complementarity-determining-1.		Complementarity-determining-1.
FT REGION 89 97 Complementarity-determining-2.		Complementarity-determining-2.
FT REGION 98 107 Complementarity-determining-3.		Complementarity-determining-3.
FT DISULFID 23 88 Complementarity-determining-4.		Complementarity-determining-4.
NON TER 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;		
SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90E4E98 CRC64;		
Query Match 83.8%; Score 467; DB 1; Length 108;		
Best Local Similarity 83.2%; Pred. No. 8 4e-39;		
Matches 89; Conservative 8; Mismatches 10; Indels 0; Gaps 0;		
Db	Db	Db
RESULT 15		
KV1_HUMAN STANDARD; PRT; 108 AA.		
ID KV1_HUMAN STANDARD; PRT; 108 AA.		
AC P01610;		
DT 21-JUL-1986 (Rel. 01, Created)		
DT 21-JUL-1986 (Rel. 01, Last sequence update)		
DT 10-MAY-2005 (Rel. 47, Last annotation update)		
DE 19 kappa chain V-I region WEA.		
OS Homo sapiens (Human)		
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC Homo.		
NCBI_TAXID=9606;		
[1]	RN	RN
PROTEIN SEQUENCE;	PUBMED=5489770;	PROTEIN SEQUENCE;
MEDLINE=71064023;	PubMed=112021;	MEDLINE=79237922;
Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.; "The primary structure of the Bence-Jones protein Rue. The amino acid sequence of the variable part of a human L-chain of the kappa-type.";	PubMed=112021;	PubMed=112021;
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-1 - MISCELLANEOUS: This is a Bence-Jones protein.		
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CC	CC	CC
DR PIR; A01870; KIHUEU.		
DR HSSP; P01607; IBWW.		
SMR; P01604; 1_108.		
GO; GO:0005576; C: extracellular region; NAS.		
GO; GO:0003823; F: antigen binding; NAS.		
GO; GO:0006955; P: immune response; NAS.		
InterPro; IPR007110; Ig-like.		
InterPro; IPR003596; Ig_v.		
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PROSITE; PS50835; Ig_LIKE_1.		
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FT REGION 89 97 Complementarity-determining-2.		Complementarity-determining-2.
FT REGION 98 107 Complementarity-determining-3.		Complementarity-determining-3.
FT DISULFID 23 88 Complementarity-determining-4.		Complementarity-determining-4.
NON TER 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;		
SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90E4E98 CRC64;		
Query Match 83.8%; Score 467; DB 1; Length 108;		
Best Local Similarity 83.2%; Pred. No. 8 4e-39;		
Matches 89; Conservative 8; Mismatches 10; Indels 0; Gaps 0;		
Db	Db	Db
RESULT 14		
KV1_HUMAN STANDARD; PRT; 108 AA.		
ID KV1_HUMAN STANDARD; PRT; 108 AA.		
AC P01604;		
DT 21-JUL-1986 (Rel. 01, Created)		
DT 21-JUL-1986 (Rel. 01, Last sequence update)		
DT 10-MAY-2005 (Rel. 47, Last annotation update)		
DE 19 kappa chain V-I region WEA.		
OS Homo sapiens (Human)		
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC Homo.		
NCBI_TAXID=9606;		
[1]	RN	RN
PROTEIN SEQUENCE;	PUBMED=5489770;	PROTEIN SEQUENCE;
MEDLINE=71064023;	PubMed=112021;	MEDLINE=79237922;
Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.; "The primary structure of the Bence-Jones protein Rue. The amino acid sequence of the variable part of a human L-chain of the kappa-type.";	PubMed=112021;	PubMed=112021;
Hoppe-Seyler's Z. Physiol. Chem. 360:734(1979).		
-1 - MISCELLANEOUS: This is a Bence-Jones protein.		
CC	CC	CC
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CC	CC	CC
DR PIR; A01870; KIHUEU.		
DR HSSP; P01607; IBWW.		
SMR; P01604; 1_108.		
GO; GO:0005576; C: extracellular region; NAS.		
GO; GO:0003823; F: antigen binding; NAS.		
GO; GO:0006955; P: immune response; NAS.		
InterPro; IPR007110; Ig-like.		
InterPro; IPR003596; Ig_v.		
SMART; SM00406; Ig_LIKE_1.		
PROSITE; PS50835; Ig_LIKE_1.		
Bence-Jones Protein; Direct protein sequencing; Immunoglobulin domain.		
KW Immunoglobulin V region.		
FT REGION 1 23 Framework-1.		Framework-1.
FT REGION 24 34 Framework-2.		Framework-2.
FT REGION 35 49 Framework-3.		Framework-3.
FT REGION 50 56 Framework-4.		Framework-4.
FT REGION 57 88 Complementarity-determining-1.		Complementarity-determining-1.
FT REGION 89 97 Complementarity-determining-2.		Complementarity-determining-2.
FT REGION 98 107 Complementarity-determining-3.		Complementarity-determining-3.
FT DISULFID 23 88 Complementarity-determining-4.		Complementarity-determining-4.
NON TER 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;		
SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90E4E98 CRC64;		
Query Match 83.8%; Score 467; DB 1; Length 108;		
Best Local Similarity 83.2%; Pred. No. 8 4e-39;		
Matches 89; Conservative 8; Mismatches 10; Indels 0; Gaps 0;		
Db	Db	Db

PROTEIN SEQUENCE.
 RX MEDLINE=832273107; PubMed=6410398;

RA Gori P, Frangione B.;
 "Amino acid sequence of the Fv region of a human monoclonal IgM
 (protein MEA) with antibody activity against 3,4-pyruvylated galactose
 in Klebsiella poly saccharides K30 and K33.",
 Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841 (1983).
 RL -1- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
 CC against 3,4-pyruvylated Galactose and isolated from a patient with
 CC Waldenstrom's macroglobulinemia.

CC This Swiss-Prot entry is copyright. It is produced through collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC DR PIR: A01876; KIHWE.
 CC DR HSSP: P03362; IWTI.
 CC DR SMR: P01610; 1-108.
 CC DR GO: GO:0005576; C extracellular region; NAS.
 CC DR GO: GO:0003823; F antigen binding; NAS.
 CC DR GO: GO:0006955; P immune response; NAS.
 CC DR InterPro: IPR07110; Ig-like.
 CC DR InterPro: IPR03536; Ig_v.
 CC DR SMART: SM00416; Ig_v.
 CC DR PROSITE: PS50935; Ig_LIKE; 1.
 CC KW Direct protein sequencing; Immunoglobulin domain;
 CC KW Immunoglobulin V region; Monoclonal antibody.
 CC FT REGION 1 23 Framework-1.
 CC FT REGION 24 34 Complementarity-determining-1.
 CC FT REGION 35 49 Framework-2.
 CC FT REGION 50 56 Complementarity-determining-2.
 CC FT REGION 57 88 Framework-3.
 CC FT REGION 89 97 Complementarity-determining-3.
 CC FT REGION 98 107 Framework-4.
 CC FT DISULFID 23 88 By similarity.
 CC FT NON TER 108 108 By similarity.
 SQ SEQUENCE 108 AA; 11840 MW; 9249B6F0945618C CRC64;
 QY Query Match Similarity 83.5%; Score 465; DB 1; Length 108;
 QY Best Local Similarity 84.1%; Pred. No. 1..7e-38;
 QY Matches 30; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGDRTITCRASQISRMLAWYQQPKRKPSLIVYASSLSQGVPS 60
 Db 1 DIQMTQSPSSLSASVGDRTITCRASQISRMLAWYQQPKRKPSLIVYASSLSQGVPS 60
 QY 61 RFSGSGSGSGDFPTLISGLQPEDFATYCCQYNSTPRTFGQGTVKIK 107
 Db 61 RFSGSGSGSGDFPTLISGLQPEDFATYCCQYNSTPRTFGQGTVKIK 107

Search completed: December 3, 2005, 14:32:20
 Job time : 189.669 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 3, 2005, 14:10:00 ; Search time 182.992 Seconds
(without alignments)
Perfect score: 557
Sequence: 1 DIQMTQSPSSLSASVGDRVTI CQQNNSYPRTFGQGTKVEIK 107
Scoring table: BL0SUM62
Gapext 0.5
Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : A_Geneseq 21:
1: geneseqP1980B:*

2: geneseqP1990B:*

3: geneseqP2000B:*

4: geneseqP2001B:*

5: geneseqP2002B:*

6: geneseqP2003AB:*

7: geneseqP2003BS:*

8: geneseqP2004B:*

9: geneseqP2005B:*

Prev. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	557	100.0	107	5 AAM48004	Aam48004 Human mon
2	557	100.0	107	8 ADR46825	Adr46825 Human ant
3	557	100.0	233	8 ADR46823	Adr46823 Human ant
4	557	100.0	411	8 ADR46829	Adr46829 Human pBl
5	538	96.6	107	4 AAB67511	Aab67511 Light cha
6	538	96.6	107	9 ADY70214	Ady70214 Human mon
7	538	96.6	108	7 ADI11407	Adi11407 18B2 anti
8	538	96.6	214	7 ADI11431	Adi11431 18B2 anti
9	537	96.4	107	9 ADY26773	Ady26773 Anti-NGF-
10	535	96.1	107	4 AAB72880	Aab72880 Human ant
11	535	96.1	107	8 AD036490	Ado36490 Human ant
12	535	96.1	107	8 AD036502	Ado36502 Human ant
13	535	96.1	107	8 ADY70210	Ady70210 Human mon
14	535	96.1	234	9 AEP48576	Aep48576 Human kap
15	535	96.1	236	9 ADV86270	Adv86270 Anti-huma
16	535	96.1	239	9 AEP48570	Aep48570 Human kap
17	535	96.1	290	9 AEP48564	Aep48564 Human kap
18	532	95.5	107	9 ADT88867	Adt88867 Human IGF
19	531	95.3	107	8 ADT88874	Adt88874 Human IGF
20	531	95.3	107	8 AEP01063	Aep01063 Human IPI
21	531	95.3	107	9 AAB72882	Aab72882 Human ant
22	530	95.2	107	4 AAB82890	Aab82890 Anti-huma
23	530	95.2	107	9 ADW07059	Adw07059 Anti-PsA
24	530	95.2	107	9	

ALIGNMENTS

RESULT 1
AAM48004
ID AAM48004 standard; protein; 107 AA.
XX
AC AAM48004;
XX
DT 08-MAR-2002 (first entry)

Human monoclonal antibody B11 variable light chain protein.
XX
DE Human monoclonal antibody B11; antigen binding portion; dendritic cell;
XX
KW Human; monoclonal antibody; B11; antigen binding portion; bacterium;
KW marnose receptor; growth; cytolysis; pathogen; virus;
KW autoimmune disease; inflammatory disorder; rheumatoid arthritis;
KW multiple sclerosis; diabetes mellitus; immunomodulatory;
KW antiinflammatory; antirheumatic; antiautomatic; neuroprotective;
KW antidiabetic; antianemia; endocrine; dermatological; antithyroid;
KW uropathic; ophthalmologic; muscular.
XX
Homo sapiens.
OS
XX
WO200185798-A2.
XX
PN
XX
PD 15-NOV-2001.
XX
PP 08-MAY-2001; 2001WO-US015114.
XX
PR 08-MAY-2000; 2000US-0203126P.
PR 07-SEP-2000; 2000US-0230739P.
XX
(MEDA-) MEDAREX INC.
PA
XX
PI Deo YM, Keler T;
XX
DR WPI; 2002-089798/12.
DR N-PSDB; ABA06023.
XX
PT New human monoclonal antibodies specific for dendritic cells, useful for
PT inhibiting growth or inducing cytosis of a dendritic cell and treating
PT or preventing a dendritic cell mediated disease, e.g., autoimmune
PT disorders.
XX
PS Example 2; Fig 13; 95pp; English.
XX
CC The invention relates to human monoclonal antibodies or their antigen
CC binding portions that specifically bind to dendritic cells and has one or
CC more of the following characteristics: (a) a binding affinity constant to
CC a dendritic cell of at least about 10 to the power 7 M-1; (b) the ability

to opsonise a dendritic cell; (c) the ability to internalise after binding to dendritic cells; or (d) the ability to activate dendritic cells. The isolated human monoclonal antibody or its antigen-binding portion may also have any of the following characteristics: (a) mediates cytolysis of dendritic cells in the presence of human effector cells; or (b) inhibit growth of dendritic cells. The antibodies or its antigen binding portion, binds to and blocks the human mannose receptor on dendritic cells. The antibodies have immunomodulatory, antiinflammatory, antidiabetic, antihypertensive, antianemic, endocrine, dermatological, antithyroid, uropathic, ophthalmological and muscular activity. The antibodies or their antigen-binding fragments are useful for inhibiting growth of a dendritic cell, inducing cytosis of a dendritic cell, treating or preventing a dendritic cell mediated disease, detecting the presence of a dendritic cell, targeting an antigen to a dendritic cell and preventing binding of pathogen's viruses or a bacterium to human mannose receptor on dendritic cells. In particular, the antibodies may be used to treat, autoimmune disease, graft versus host disease, immune system or inflammatory disorders (e.g. rheumatoid arthritis), multiple sclerosis, diabetes mellitus, myasthenia gravis, pernicious anemia, Addison's disease, lupus erythematosus, Reiter's syndrome and Graves disease. The present sequence is that of the human monoclonal antibody B11 variable light chain, useful to the invention Sequence 107 AA;

Query Match Score 557; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 5e-36;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIQMTOQSPSSLSASVGDRVTITCRASQISIRWLAMYQQPKPEKAPSLIYAAASSLQSVPDS 60
Db 1 DIQMTOQSPSSLSASVGDRVTITCRASQISIRWLAMYQQPKPEKAPSLIYAAASSLQSVPDS 60
Qy 61 RFSGGSGSGTDFLTISGLQPEDFATYYCQQYNSTPRTFGGTKVBIK 107
Db 61 RFSGGSGSGTDFLTISGLQPEDFATYYCQQYNSTPRTFGGTKVBIK 107

RESULT 2
ID ADR46825
AC ADR46825;
DT 18-NOV-2004 (first entry)
XX Human antibody B11 light chain variable region protein SEQ ID NO:8.
XX molecular conjugate; monoclonal antibody; human antigen presenting cell; betahCG; beta chorionic gonadotropin; antibody; T cell-mediated immune response; immunisation; cytostatic; antimicrobial; immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial; CDB agonist; vaccine; autoimmune disorder; cancer; infectious disease; melanoma; fibrosarcoma; leukemia; HIV; hepatitis; malaria; herpes; antibody B11; light chain variable region.
XX Homo sapiens.
PN WO2004074432-A2.
XX PD 02-SEP-2004.
XX PP 30-JAN-2004; 2004WO-US002725.
PR 31-JAN-2003; 2003US-0443979P.
XX PA (MEDA-) MEDAREX INC.
XX PI Keler T, Endres M, He L, Ramakrishna V;
DR WPI: 2004-635555/61.
DR N-PSDB, ADR46824.

CC New molecular conjugate having a monoclonal antibody that binds to human PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a PT cytotoxic T cell response in cancers and infectious diseases.
XX Clatn 11; SEQ ID NO 8; 82pp; English.

XX The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (APCs) linked to beta human chorionic gonadotropin (betahCG), where the antibody comprises a heavy and/or light chain variable region derived from a human VH5-51 or VK-L15 germline sequence with the 98 or 95 amino acid sequences of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are linked to betahCG; (2) a molecular conjugate comprising a human single chain antibody that binds to human APCs linked to betahCG, where the conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46822); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an adjuvant; (4) inducing or enhancing a T cell-mediated immune response, against betahCG, comprising contacting any of the molecular conjugates described above with APCs such that the antigen is processed and presented to T cells in a manner which induces or enhances a T cell-mediated response against the antigen; (5) immunising a subject comprising administering any of the molecular conjugates described above, optionally in combination with an adjuvant, cytokine which stimulates proliferation of dendritic cells and/or an immunostimulatory agent; and (6) inducing or enhancing a cytotoxic T cell response against an antigen, comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either in vivo or ex vivo with APCs such that the antigen is internalised, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate has cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic, virucide and antimalarial activities, and can be used as a CDB agonist, and in vaccines. The methods and compositions of the present invention are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents a human antibody B11 light chain variable region, which is used in the exemplification of the present invention.

XX SQ Sequence 107 AA;
Query Match Score 557; DB 8; Length 107;
Best Local Similarity 100.0%; Pred. No. 5e-36;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISIRWLAMYQQPKPEKAPSLIYAAASSLQSVPDS 60
Db 1 DIQMTQSPSSLSASVGDRVTITCRASQISIRWLAMYQQPKPEKAPSLIYAAASSLQSVPDS 60
Qy 61 RFSGGSGSGTDFLTISGLQPEDFATYYCQQYNSTPRTFGGTKVBIK 107
Db 61 RFSGGSGSGTDFLTISGLQPEDFATYYCQQYNSTPRTFGGTKVBIK 107

RESULT 3
ID ADR46823
AC ADR46823;
DT 18-NOV-2004 (first entry)
XX DE Human antibody B11 light chain variable region protein SEQ ID NO:6.
XX KW molecular conjugate; monoclonal antibody; human antigen presenting cell; betahCG; beta chorionic gonadotropin; antibody; T cell-mediated immune response; immunisation; cytostatic; antimicrobial; KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial; KW CDB agonist; vaccine; autoimmune disorder; cancer; infectious disease; KW melanoma; fibrosarcoma; leukemia; HIV; hepatitis; malaria; herpes; antibody B11; light chain variable region.
XX OS Homo sapiens.
PN WO2004074432-A2.
XX PD 02-SEP-2004.
XX PP 30-JAN-2004; 2004WO-US002725.
PR 31-JAN-2003; 2003US-0443979P.
XX PA (MEDA-) MEDAREX INC.
XX PI Keler T, Endres M, He L, Ramakrishna V;
DR WPI: 2004-635555/61.
DR N-PSDB, ADR46824.

KW	T cell-mediated immune response; immunisation; cytosstatic; antimicrobial; immunosuppressive; anti-HIV; hepatotropic; antimalarial;					
KW	CDB agonist; vaccine; autoimmune disorder; cancer; infectious disease; melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;					
KW	antibody B11; light chain variable region.					
XX	Homo sapiens.					
XX	PN WO2004074432-A2.					
XX	PD 02-SEP-2004.					
XX	PP 30-JAN-2004; 2004WO-US002725.					
XX	PR 31-JAN-2003; 2003US-0443979P.					
XX	(MEDA-) MEDAREX INC.					
PA	XX					
PA	PI Keler T, Endres M, He L, Ramakrishna V;					
XX	XX DR WPI; 2004-635555/61.					
XX	DR N-PSDB; ADR46022.					
PT	PT New molecular conjugate having a monoclonal antibody that binds to human Apces linked to a beta human chorionic gonadotropin, useful for inducing a cytotoxic T cell response in cancers and infectious diseases.					
XX	PS Claim 14; SEQ ID NO 6; 82pp; English.					
XX	CC The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (APCs) linked to beta human chorionic gonadotropin (betahCG), where the antibody comprises a heavy and/or light chain variable region derived from a human VH5-51 or VK-115 germline sequence with the 98 or 95 amino acid sequences of SEQ ID NO:10 or 32 (ADR46847, or ADR46849), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are linked to betahCG; (2) a molecular conjugate comprising a human single chain antibody which binds to human APCs linked to betahCG, where the conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an adjuvant; (4) inducing or enhancing a T cell-mediated immune response, against betahCG, comprising contacting any of the molecular conjugates described above with APCs such that the antigen is processed and presented to T cells in a manner which induces or enhances a T cell-mediated response against the antigen; (5) immunising a subject comprising administering any of the molecular conjugates described above, optionally in combination with an adjuvant, a cytokine which stimulates proliferation of dendritic cells and/or an immunostimulatory agent; and (6) inducing or enhancing a cytotoxic T cell response against an antigen, comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either in vivo or ex vivo with APCs such that the antigen is internalised, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate has cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic, virucide and antimalarial activities, and can be used as a CD8 agonist, and in vaccines. The methods and compositions of the present invention are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents a human antibody B11 light chain variable region, which is used in the exemplification of the present invention.					
SQ	Sequence 233 AA;	100.0%;	Score 557;	DB 8;	Length 233;	
		100.0%;	pred. No. 1e-35;	Mismatches 0;	Indels 0;	Gaps 0;

RESULT 4	
Qy	1 DIQMTQSPSSLSASVGDRTVTITCRASOGISRMLAQNQQKPKAKPSLIVAAASSI-LQSGVPY 60 20 DIQMTQSPSSLSASVGDRTVTITCRASOGISRMLAQNQQKPKAKPSLIVAAASSI-LQSGVPY 79
Db	61 RFSGSGSGTDFITLITLQSPDFTATYCQQINSYPRTFGGQTKEIK 107 80 RFSGSGSGTDFITLITLQSPDFTATYCQQINSYPRTFGGQTKEIK 126
Qy	Human pb11-betaHCG molecular conjugate protein SEQ ID NO:12.
Db	XX XX DE Human pb11-betaHCG molecular conjugate protein SEQ ID NO:12. XX XX KW molecular conjugate; monoclonal antibody; human antigen presenting cell; KW antigen presenting cell; APC; human; beta human chorionic gonadotropin; KW betahCG; beta chorionic gonadotropin; antibody; KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial; KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial; KW C18 agonist; vaccine; autoimmune disorder; cancer; infectious disease; KW melanoma; fibroarcoma; leukaemia; HIV; hepatitis; malaria; herpes; KW antibody B11; pb11-betaHCG molecular conjugate; fusion protein. XX OS Homo sapiens. OS Synthetic. XX PN WO2004074432-A2. XX PD 02-SEP-2004. XX PF 30-JAN-2004; 2004WO-US0002725. XX PR 31-JAN-2003; 2003US-0443979P. XX PA (MEDA -) MEDAREX INC. XX PI Keler T, Endres M, He I, Ramakrishna V; XX DR WPI: 2004-6315555/61. DR N-PSDB; ADR16828. XX PT New molecular conjugate having a monoclonal antibody that binds to human PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a PT cytotoxic T cell response in cancers and infectious diseases. XX PS SEQ ID NO 12; 82pp; English. XX CC The present invention describes a molecular conjugate comprising a CC monoclonal antibody that binds to a human antigen presenting cell (APCs) CC linked to beta human chorionic gonadotropin (betaHCG), where the antibody CC comprises a heavy and/or light chain variable region derived from a human CC VH5-51 or VK-L15 germline sequence with the 98 or 95 amino acid sequence CC of SEQ ID NO: 30 or 32 (ADR16847, or ADR16849), respectively. Also CC described: (1) a molecular conjugate comprising a human antibody heavy CC chain and a human antibody light chain, where either or both chains are CC linked to betaHCG; (2) a molecular conjugate comprising a human single CC chain antibody that binds to human APCs linked to betaHCG, where the CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 CC (ADR16829); (3) a composition comprising any of the molecular conjugates CC as described above, and a carrier, optionally in combination with an CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response, CC against betahCG, comprising contacting any of the molecular conjugates CC described above with APCs such that the antigen is processed and CC presented to T cells in a manner which induces or enhances a T cell- CC mediated response against the antigen; (5) immunising a subject CC comprising administering any of the molecular conjugates described above CC optionally in combination with an adjuvant, a cytoimmunulatory agent; and CC proliferation of dendritic cells and/or an immunostimulatory agent; and CC

(6) inducing or enhancing a cytotoxic T cell response against an antigen, comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either *in vivo* or *ex vivo* with APCs such that the antigen is internalised, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate has cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic, virucidal and antimalarial activities, and can be used as a CD8 agonist, and in vaccines. The methods and compositions of the present invention are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by eliciting potent antigen specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents a human PB11-beta and G molecular conjugate, which is used in the exemplification of the present invention.

SQ Sequence 411 AA;

Query Match 100.0%; Score 557; DB 8; Length 411;
 Best Local Similarity 100.0%; Pred. No. 1.8e-35;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 79

Qy 61 RFSGSGSGIDFTLTISGLQPEDFATYYCQOYNSTYPRTEFGQTKVIK 107
 Db 80 RFSGSGSGIDFTLTISGLQPEDFATYYCQOYNSTYPRTEFGQTKVIK 126

RESULT 5

AAB67511 standard peptide; 107 AA.

AC AAB67511;

XX 29-MAY-2001 (first entry)

XX Light chain variable region of anti-CTLA-4 antibody 1E2.

XX Complementarity determining region; CDR; immune response; antibody; cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer; autoimmune disease; infection; disease; inflammation; allergy; rheumatoid arthritis; myasthenia gravis; lupus erythematosus; multiple sclerosis; insulin-dependent diabetes mellitus; inflammation; transplant rejection; graft versus host disease.

OS Homo sapiens.

XX Key Location/Qualifiers

PT Region 24 .34 /note= "CDR1"

PT Region 50 .66 /note= "CDR2"

PT Region 89 .97 /note= "CDR3"

XX PN WO200114424-A2. /label= CDR1

XX PD 01-MAR-2001. /note= "complementarity determining region"

XX PT 24-AUG-2000; 2000WO-US023356. /label= CDR2

XX PR 24-AUG-1999; 99US-0150452P. /note= "complementarity determining region"

XX PA (MEDA-) MEDAREX INC. /label= CDR3

XX PI Korman AJ, Halk EL, Lonberg N, /note= "complementarity determining region"

XX DR WPI: 2001-202933/20. /label= CDR3

XX PT Novel human sequence antibody that binds to human cytotoxic T lymphocyte /note= "complementarity determining region"

associated antigen-4, useful for inducing, augmenting or prolonging immune response to antigen or for suppressing immune response in patient.

PT PS XX Claim 27; Fig 7; 127PP; English.

The present sequence represents the light chain variable region of human antibody 1E2. This antibody specifically binds to human cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such antibodies are used in methods for inducing, augmenting or prolonging an immune response to an antigen in a patient, where the antibodies block binding of human CTLA-4 to human B7 ligands. The antibodies are also useful for treating autoimmune disease in a subject caused or exacerbated by increased activity of T cells and for treating prostate cancer, melanoma or epithelial cancer. A polyclonal or polyclonal antibody preparation comprising two antibodies of the invention are useful for suppressing a immune response in a patient. They are used for treating cancer, infectious diseases and promoting beneficial autoimmune reactions for the treatment of diseases with inflammatory or allergic components. The polyclonal or polyclonal preparations are useful for treating autoimmune diseases such as rheumatoid arthritis, myasthenia gravis and lupus erythematosus; multiple sclerosis; insulin-dependent diabetes mellitus; transplant rejection; and inflammation, graft versus host disease.

SQ Sequence 411 AA;

Query Match 100.0%; Score 557; DB 8; Length 411;
 Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 79

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60

SQ Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34; Mismatches 3; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60
 Db 20 DIQMTQSPSSLSASVGDRVTITCRASQISRMLAWYQQKPEKAPSLIYASSLQSGVPS 60</p

PR	16-OCT-2003; 2003US-0512336P.	Qy	61 RFSGSGSGTDFLTISLQPEDFATYYCQOYNSYRTFGQGTKVIEK 107
XX	(MEDA-) MEDAREX INC.	Db	61 RFSGSGSGTDFLTISLQPEDFATYYCQOYNSYRTFGQGTKVIEK 107
PA			
PI	Keler T, Blanset D, Vitale LA, Lowy I, Srinivasan M;	RESULT 7	
XX	WPI: 2005-214725/22.	ID ADF11407	ADFE11407 standard; protein; 108 AA.
DR	N-PSDB; ADY70213.	XX	XX
XX	New human monoclonal antibody that binds to Bacillus anthracis protective antigen and neutralizes a Bacillus anthracis toxin, useful in preparing a composition for treating or preventing anthrax infection.	PT	12-FEB-2004 (First entry)
XX	PS SEQ ID NO 18; 119pp; English.	DE	18B2 anti-OPGL antibody kappa chain variable region SEQ ID NO:20.
XX	This invention describes a novel human monoclonal antibody which binds to Bacillus anthracis protective antigen with an affinity of at least 10 ⁻⁷ M ⁻¹ and neutralizes a Bacillus anthracis lethal factor toxin at an ED ₅₀ of 5 microg/ml or less in a toxin neutralization assay. The invention also describes: 1) an expression vector; 2) a transfectoma comprising the expression vector; 3) a transgenic non-human animal that expresses the human monoclonal antibody and that has a genome comprising a human heavy chain transgene or transchromosome and a human light chain transgene or transchromosome; 4) an immunoconjugate comprising the human monoclonal antibody, linked to a therapeutic agent chosen from a cytotoxin or radioisotope; 5) a pharmaceutical composition comprising the immunocomjugate or human monoclonal antibody and a carrier or an additional therapeutic agent, comprising a protective antigen vaccine or a second antibody against anthrax bacteria, spores, lethal factor or edema factor, Fab, F(ab') ₂ , Fv or single chain Fv fragment of the second antibody; 6) a hybridoma that produces a detectable amount of the human monoclonal antibody; 7) a method of producing the human monoclonal antibody; 8) a method of inhibiting a physiological activity of Bacillus anthracis protective antigen in a cell susceptible to anthrax infection; 9) a method of neutralizing a Bacillus anthracis toxin in a cell susceptible to anthrax infection comprising immunizing the transgenic non-human animal with Bacillus anthracis protective antigen or a cell expressing Bacillus anthracis protective antigen, so that antibodies are produced by B cells of the animal, isolating B cells of the animal and fusing the B cells with myeloma cells to form immortal hybridoma cells that secrete the antibody; 10) a method of treating or preventing anthrax infection in a host infected with Bacillus anthracis; 11) a method of detecting the presence of Bacillus anthracis protective antigen in a sample; 12) a method of treating or preventing anthrax infection in a patient; and 13) a method of screening for an antibody against anthrax protective antigen. The human monoclonal antibody comprises human IgG1 or IgG3 heavy chain variable region and a human kappa light chain variable and their conservative sequence modifications. The human monoclonal antibody is a Fab fragment or a single chain antibody (scFv) and is produced by a hybridoma, which is prepared from a B cell obtained from a transgenic non-human animal having a genome comprising a human heavy chain transgene or transchromosome and a human light chain transgene or transchromosome fused to an immortalized cell. The heavy or light chain variable region comprises CDR1, FR2, CDR2, FR3, CDR3 or FR4. The heavy chain variable region having FR1, FR2, FR3 or FR4 sequences are derived from the human heavy chain VH3-33 or VH3-7 germline sequences. The light chain variable region having FR1, FR2, FR3 or FR4 sequences are derived from the human light chain L15, L18 or A27 germline sequences. The ability of the antibody to neutralize the toxin requires binding to Fc receptor. This sequence represents the human monoclonal antibody SDS variable region light chain comprising a L15 V-segment and a JK4 J-segment.	XX	AC ADF11407;
XX	Sequence 107 AA;	XX	XX
XX	Query Match 96.6%; Score 538; DB 9; Length 107;	DT	12-FEB-2004 (First entry)
XX	Best Local Similarity 97.2%; Pred. No. 1.5e-34;	XX	XX
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	Db	1 DIQMTOQSPSSLSASVGRVTITCRASCGISRWLAWQQKPEKAPSKLIYAASSLQGVPS 60	
Qy 1 DIQMTOQSPSSLSASVGRVTITCRASCGISRWLAWQQKPEKAPSKLIYAASSLQGVPS 60	Qy	61 RFSGSGSGTDFLTISLQPEDFATYYCQOYNSYRTFGQGTKVIEK 107	
Db 1 DIQMTOQSPSSLSASVGRVTITCRASCGISRWLAWQQKPEKAPSKLIYAASSLQGVPS 60	Db	61 RFSGSGSGTDFLTISLQPEDFATYYCQOYNSYRTFGQGTKVIEK 107	

RESULT 8
 ADP11431
 ID ADP11431 standard; protein; 214 AA.
 XX
 AC ADP11431;
 XX DT 12-FEB-2004 (first entry)
 XX DE 18B2 anti-OPGL antibody light chain SEQ ID NO:44.
 XX human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
 XX osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
 XX osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.
 XX OS Homo sapiens.
 XX PN WO2003086289-A2.
 XX PD 23-OCT-2003.
 XX PP 07-APR-2003; 2003WO-US010749.
 XX PR 05-APR-2002; 2002US-0370407P.
 XX PA (AMGB-) AMGEN INC.
 XX PI Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;
 XX DR 2003-845253/78.
 XX PR 05-APR-2002; 2002US-0370407P.
 XX PA (AMGB-) AMGEN INC.
 XX PT New isolated antibody that specifically binds osteoprotegerin ligand,
 PT useful for diagnosing or treating bone disorders, such as osteoporosis,
 PT bone loss from arthritis, Paget's disease or osteopenia.
 XX PS Claim 18; SEQ ID NO 44; 156pp; English.
 XX
 The present invention describes an isolated human antibody (I) that
 specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
 pharmaceutical composition comprising a pharmaceutical carrier and a
 therapeutic amount of (I); (2) methods of treating an osteopenic disorder
 in a patient, comprising administering to a patient the pharmaceutical
 composition of (1) or a pharmaceutical amount of (I); and (3) a method
 for detecting OPGL in a biological sample, comprising contacting the
 sample with (1) under conditions that allow for binding of the antibody
 to OPGL, and measuring the level of bound antibody in the sample. (1) has
 osteopathic, antiarthritic and cytostatic activities, and can be used in
 gene therapy. The composition and methods are useful in diagnosing or
 treating bone disorders, such as osteoporosis, bone loss from arthritis,
 Paget's disease or osteopenia. The antibody (I) may also be used for
 detecting OPGL in biological samples and in identifying cells or tissues
 that produce the protein. The present sequence represents a sequence
 which is used in the exemplification of the present invention.
 XX Sequence 214 AA;
 Query Match 96.6%; Score 538; DB 7; Length 214;
 Best Local Similarity 97.2%; Pred. No. 2.9e-34;
 Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 SQ 1 DIQMTQSPSSLSASVGDRITCRASQIGISRSWLAQYQQKPEKAPSILYAASSLQSGVPS 60
 Db 1 DIQMTQSPSSLSASVGDRITCRASQIGISRSWLAQYQQKPEKAPSILYAASSLQSGVPS 60
 Qy 61 RFSGSGSGTGTDFLTISGLOPEDFATYCOQNSYPRTFGQGTKVIEK 107
 Db 61 RFSGSGSGTGTDFLTISGLOPEDFATYCOQNSYPRTFGQGTKVIEK 107
 Qy 1 DIQMTQSPSSLSASVGDRITCRASQIGISRSWLAQYQQKPEKAPSILYAASSLQSGVPS 60
 Db 1 DIQMTQSPSSLSASVGDRITCRASQIGISRSWLAQYQQKPEKAPSILYAASSLQSGVPS 60
 Qy 61 RFSGSGSGTGTDFLTISGLOPEDFATYCOQNSYPRTFGQGTKVIEK 107

Ddb	61	RFGSGSGSGTDFLTISLQPEDFATYQQVNSYPMTFGQGTKVBIK	107	
	RESULT 10			
	AAB72880	AAB72880 standard; protein: 107 AA.		
	AAB72880;			
	10-MAY-2001	(first entry)		
	Human anti-HER2/neu antibody 3-F2 light chain.			
	XX	XX		
	Human: HER2; neu; erbB2; oncogene; cancer; antibody; immunotherapy; 3-F2;			
	1-D2; 2-E8; growth factor receptor.			
	XX	XX		
	Homo sapiens.			
	XX	XX		
	WO200109187-A2.			
	XX	XX		
	08-FEB-2001.			
	XX	XX		
	25-JUL-2000; 2000WO-US020272.			
	XX	XX		
	PR 29-JUL-1999; 99US-0146313P.			
	10-MAR-2000; 2000US-0188539P.			
	XX	XX		
	PA (MEDA-) MEDAREX INC.			
	XX	XX		
	Keler T, Deo Y;			
	XX	XX		
	WPI: 2001-168698/17.			
	N-PSDB; AAF75586.			
	XX	XX		
	New human monoclonal antibody that specifically binds to growth factor receptor HER2/neu, for treating, preventing or diagnosing diseases characterized by aberrant HER2/neu expression e.g. cancers.			
	XX	XX		
	Disclosure; Page 104-105; 113pp; English.			
	XX	XX		
	The present invention provides the protein and coding sequences for human monoclonal antibodies which bind specifically to the HER2/neu growth factor receptor (also known as erbB2). These are designated 3-F2, 1-D2 and 2-E8. They can be used in the immunotherapy-based treatment and prognosis of cancers, particularly adenocarcinomas such as salivary gland, stomach, kidney, mammary gland, lung and squamous cell carcinomas, and ovarian cancer. The present sequence is part of an antibody of the invention			
	XX	XX		
	Sequence 107 AA;			
	SQ	Score 535; DB 4; Length 107;		
	Best Local Similarity 96.3%; Pred. No. 2, 6e-34; Indels 0; Gaps 0;			
	Matches 103; Conservative 1; Mismatches 1; Gaps 0;			
	XX	Sequence 107 AA;		
	SQ	Score 535; DB 8; Length 107;		
	Best Local Similarity 96.3%; Pred. No. 2, 6e-34; Indels 0; Gaps 0;			
	Matches 103; Conservative 1; Mismatches 1; Gaps 0;			
	Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRLAWYQKPEAKPKSLIYAASSLQSGVPS 60			
	Db 1 DIQMTQSPSSLSASVGDRVTITCRASQISRLAWYQKPEAKPKSLIYAASSLQSGVPS 60			
	Qy 61 RFSGSGSGTDFLTISLQPEDFATYQQVNSYPMTFGQGTKVBIK 107			
	Db 61 RFSGSGSGTDFLTISLQPEDFATYQQVNSYPMTFGQGTKVBIK 107			
	RESULT 11			
	AD036490	Human anti-heparanase 2HB Wk amino acid sequence SEO ID NO:4.		
	XX	AC AD036490;		
	XX	12-AUG-2004 (first entry)		
	DE			
	RESULT 12			
	ADO16502			
	ID ADO16502	standard; protein: 107 AA.		
	XX			
	AC ADO16502;			
	AC ADO16502			

XX DT 12-AUG-2004 (first entry)
 XX ID ADO36494 standard; protein; 107 AA.
 DB XX
 AC XX
 ADO36494;
 XX DT 12-AUG-2004 (first entry)
 Human anti-heparanase 22D9 V_k amino acid sequence SEQ ID NO:8.
 XX human; monoclonal antibody; heparanase; heparanase inhibitor;
 anti-heparanase antibody; cytosatic; immunosuppressive; antiarthritic;
 antiasthmatic; antiinflammatory; dermatological; antiarteriosclerotic;
 neuroprotective; nontropic; heparanase antagonist; cancer; Tumour;
 melanoma; lymphoma; prostate carcinoma; pancreatic carcinoma;
 bladder carcinoma; fibrosarcoma; rhabdomyosarcoma; mastocytoma;
 mammary adenocarcinoma; leukaemia; leukemoid fibroblast;
 autoimmune disease; arthritis; asthma; lupus erythematosus;
 allograft rejection; vascular restenosis; atherosclerosis;
 Alzheimer's disease.
 XX OS Homo sapiens.
 PN WO2004043989-A2.
 PD XX
 Homo sapiens.
 XX WO2004043989-A2.
 PN XX
 PR 05-NOV-2003: 2003WO-US035464.
 XX XX
 PR 07-NOV-2002: 2002US-0424803P.
 XX XX
 PR 27-MAY-2004.
 PA (MEDA-) MEDAREX INC.
 PA (CELL-) CELLTECH R & D.
 PR 05-NOV-2003: 2003WO-US035464.
 XX XX
 PR 07-NOV-2002: 2002US-0424803P.
 XX XX
 PA (MEDA-) MEDAREX INC.
 PA (CELL-) CELLTECH R & D.
 PR 05-NOV-2003: 2003WO-US035464.
 XX XX
 PR 07-NOV-2002: 2002US-0424803P.
 XX XX
 PT Huang H, Holmes S, Mason S;
 PT DR WPI: 2004-411694/38.
 PT N-PDBB; ADO36501.
 PT DR WPI: 2004-411694/38.
 PT N-PDBB; ADO36501.
 XX XX
 PT New human monoclonal antibody to heparanase, for use in treating or
 preventing cancer, autoimmune disease, arthritis, asthma, lupus
 erythematosus, allograft rejection, atherosclerosis, and Alzheimer's
 disease.
 XX PS Claim 47; SEQ ID NO 16; 108pp; English.
 XX The present invention describes an isolated human monoclonal antibody
 which binds to and inhibits activity of human heparanase. Human anti-
 heparanase antibodies of the present invention have cytosatic,
 immunosuppressive, antiarthritic, antiinflammatory, antiasthmatic,
 dermatological, antiarteriosclerotic, neuroprotective and nontropic
 activities, and can be used as heparanase antagonists. The antibody
 methods and compositions of the present invention are useful in treating
 or preventing cancer or tumours, e.g. melanoma, lymphoma, prostate
 carcinoma, pancreatic carcinoma, bladder carcinoma, fibrosarcoma,
 rhabdomyosarcoma, mastocytoma, leukaemia or a
 rheumatoid fibroblast, autoimmune disease, arthritis, asthma, lupus
 erythematosus, allograft rejection, vascular restenosis, atherosclerosis,
 and Alzheimer's disease. The present sequence represents a human anti-
 heparanase 5G10 V_k amino acid sequence, which is used in the
 exemplification of the present invention.
 XX Sequence 107 AA;
 SQ Query Match 96.1%; Score 535; DB 8; Length 107;
 Best Local Similarity 96.3%; Pred. No. 2.6e-34;
 Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Sequence 107 AA;
 XX Query Match 95.1%; Score 535; DB 8; Length 107;
 Best Local Similarity 96.3%; Pred. No. 2.6e-34;
 Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 SQ 1 DIQMTQSPSSLSASVGDRVTITCRASQISRLWYQQKPEAKPLIVASSLQGVPS 60
 Db 1 DIQMTQSPSSLSASVGDRVTITCRASQISWLWYQQKPEAKPLIVASSLQGVPS 60
 Qy 61 RPSSGSQGTDTLTLTSGLOPEDFATTYQQQNSYPRFTGGTQTKVIK 107
 Db 61 RPSSGSQGTDTLTLTSGLOPEDFATTYQQQNSYPRFTGGTQTKVIK 107
 Qy 1 DIOQMTQSPSSLSASVGDRVTITCRASQISRLWYQQKPEAKPLIVASSLQGVPS 60
 Db 1 DIOQMTQSPSSLSASVGDRVTITCRASQISWLWYQQKPEAKPLIVASSLQGVPS 60
 Qy 61 RFSGSGSGGTDTLTLTSGLOPEDFATTYQQQNSYPRFTGGTQTKVIK 107
 Db 61 RFSGSGSGGTDTLTLTSGLOPEDFATTYQQQNSYPRFTGGTQTKVIK 107

Db 61 RFSGSGSGTDFLTISLQPEDFATYYCQQVNSPYTFGGSTKLEIK 107
RESULT 14
AC AEB48576; **ID AEB48576 standard; protein; 234 AA.**
XX DT 06-OCT-2005 (first entry)
DB Human kappa light chain-TAKA signal peptide fusion protein.
XX KW monoclonal antibody; antibody production; light chain; alpha amylase; TAKA; fusion protein.
XX OS Homo sapiens.
OS Aspergillus oryzae.
PN WO2005070962-A1.
XX PD 04-AUG-2005.
XX PF 20-JAN-2005; 2005WO-DK0000035.
XX PR 21-JAN-2004; 2004DK-00000077.
PR 05-FEB-2004; 2004DK-00000174.
PR 12-MAY-2004; 2004DK-000000761.
PA (NOVO) NOVOZYMES AS.
XX PI Lehmbbeck J, Wahlbom F;
XX DR WPI: 2005-533997/54.
XX PT Producing a monoclonal antibody by providing a heterokaryon fungus comprising a first nucleus and a second nucleus and culturing the heterokaryon fungus for expression of antibody light and heavy chains.
XX PS Example 9; SEQ ID NO 25; 94pp; English.
XX CC The invention describes a method of producing a monoclonal antibody comprising providing a heterokaryon fungus comprising a first nucleus comprising a sequence encoding a light chain of an antibody, and a second nucleus comprising a sequence encoding a heavy chain of an antibody, and culturing the heterokaryon fungus for expression of the antibody light and heavy chains. Also described are: a nucleic acid construct comprising a first nucleic acid sequence encoding a light chain of an antibody and a third nucleic acid sequence encoding a signal peptide heterologous to the first nucleic acid sequence; a nucleic acid construct comprising a first nucleic acid sequence encoding a heavy chain of an antibody and a third nucleic acid sequence encoding a signal peptide heterologous to the first nucleic acid sequence; a nucleic acid construct comprising a first nucleic acid sequence encoding a light chain of an antibody and a second nucleic acid sequence encoding a cellulose binding domain; a nucleic acid construct comprising a first nucleic acid sequence encoding a heavy chain of an antibody and a second nucleic acid sequence encoding a cellulose binding domain comprising a cellulose binding domain; a heterokaryon fungal host cell comprising a first nucleus and a second nucleus, where the first nucleus comprises a first nucleic acid construct comprising a first nucleic acid sequence encoding a light chain of an antibody, and the second nucleus comprises a second nucleic acid construct comprising a first nucleic acid sequence encoding a heavy chain of an antibody, and where at least one of the nucleic acid constructs further comprises a second nucleic acid sequence encoding a heteroprotein or a functional part comprising a first nucleus and a second nucleus, where the first nucleus comprises a first nucleic acid construct comprising a first nucleic acid sequence encoding a light chain of an antibody, and the second nucleus comprises a second nucleic acid construct comprising a first nucleic acid sequence encoding a heavy chain of an antibody, and where at least one of the nucleic acid constructs further comprises a third nucleic acid sequence encoding a signal peptide heterologous to the first nucleic acid sequence. The method is useful for

CC producing monoclonal antibodies in heterokaryon fungus or in fungal host cells. This is the amino acid sequence of a fusion protein comprising human kappa light chain in which the native signal sequence has been replaced with the alpha amylase (TAKA) signal peptide.
XX SQ Sequence 234 AA;
Query Match 96.1%; Score 535; DB 9; Length 234;
Best Local Similarity 96.3%; Pred. No. 5.4e-34;
Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX Qy 1 DIQMTPSPSSLSASGDRVTITCRASQISRWLWYQQREPKAPSLLIVASSLSQGVPS 60
Db 21 DIQMTPSPSSLSASGDRVTITCRASQISSWLWYQQREPKAPSLLIVASSLSQGVPS 80
XX Qy 61 RFSGSGSGTDFLTISLQPEDFATYYCQQVNSPYTFGGSTKLEIK 107
Db 81 RFSGSGSGTDFLTISLQPEDFATYYCQQVNSPYTFGGSTKLEIK 127
RESULT 15
ADV86270
ID ADV86270 standard; protein; 236 AA.
XX XX ADV86270;
AC AC
XX XX DT 24-FEB-2005 (first entry)
XX DE Anti-human CTGF monoclonal antibody mab1 light chain protein.
XX XX antibody engineering; immunotherapy; antibody; immunotherapy; immunoglobulin; hypertension; antidiabetic; connective tissue growth factor; immunoglycemia; antidiabetic; hypotensive; cardiovascular disease; diabetes; metabolic disorder; endocrine disorder; arthritis; antiarthritic; inflammation; congestive heart failure; arthritis; antiarthritic; neoplasm.
XX KW anti-human CTGF monoclonal antibody mab1 light chain protein.
XX KW antibody engineering; immunotherapy; antibody; immunoglobulin; hypertension; antidiabetic; connective tissue growth factor; immunoglycemia; antidiabetic; hypotensive; cardiovascular disease; diabetes; metabolic disorder; endocrine disorder; arthritis; antiarthritic; inflammation; congestive heart failure; arthritis; antiarthritic; neoplasm.
XX KW anti-inflammatory; cancer; cytostatic; neoplasm.
XX OS Homo sapiens.
XX XX US2004248206-A1.
PN PN US2004248206-A1.
XX XX PD 09-DEC-2004.
XX XX PP 01-JUN-2004; 2004US-00858186.
PR 04-JUN-2003; 2003US-0475598P.
XX PA (LIN/A) LIN A Y.
CC (NEFF/T) NEFF T B.
CC (OLIV/N) OLIVER N A.
CC (USIN/W) USINGER W R.
CC (WANG/Q) WANG Q.
CC (YEOW/D) YEOWELL D A.
CC Lin AY, Neff TB, Oliver NA, Usinger WR, Wang Q, Yeowell DA;
CC PI DR N-PSDB; ADV86269.
CC XX DR N-PSDB; ADV86269.
CC XX PS Claim 32; SEQ ID NO 20; 54pp; English.
CC XX The invention relates to an isolated antibody or its fragment that specifically binds to connective tissue growth factor (CTGF) polypeptide having at least a portion of sequence of 62 amino acids fully defined in specification, or of an orthologous polypeptide derived from non-human CC species, having immunoglobulin sequence of 469 or 236 amino acids fully CC defined in specification, or antibody produced by cell line identified by CC ATCC accession number PTA-6006. (I) is useful for neutralizing an

CC activity associated with CTGF, which involves contacting (I) with a CTGF
 CC polypeptide in vitro or in vivo in a subject, under conditions suitable
 CC for formation of a complex comprising the antibody and the CTGF
 CC polypeptide, thus neutralizing the activity associated with CTGF. The
 CC subject has hypertension, hyperglycemia, diabetes, congestive heart
 CC failure, arthritis, and local or systemic inflammation. The subject has
 CC or is at risk for having a CTGF-associated disorder such as cancer. The
 CC cancer is chosen from acute lymphoblastic leukemia, dermatofibromas,
 CC breast cancer, breast carcinoma desmoplasia, angiomyoma, angiolipoma,
 CC desmoplastic cancer, prostate cancer, ovarian cancer, colorectal cancer,
 CC pancreatic cancer, gastrointestinal cancer, and liver cancer. The CTGF-
 CC associated disorder is a fibrotic disorder chosen from idiopathic
 CC pulmonary fibrosis, kidney fibrosis, glomerularclerosis, ocular
 CC fibrosis, osteoarthritis, scleroderma, cardiac fibrosis, or liver
 CC fibrosis. (I) is useful for treating or preventing a CTGF-associated
 CC disorder in a subject having or at risk for having the disorder, which
 CC involves administering (I) to the subject. The subject is at risk due to
 CC a condition chosen from hypertension, hyperglycemia, diabetes, myocardial
 CC infarction, arthritis, and inflammation. The CTGF-associated disorder is
 CC chosen from diabetic nephropathy, diabetic retinopathy, and diabetic
 CC cardiovascular disease, or cancer. (II) is useful for treating CTGF-
 CC associated disorders (claimed). (I) is useful for quantitatively and
 CC qualitatively detecting CTGF in a sample, diagnosing disease or disorder
 CC associated with CTGF, identifying whether or not an individual has a
 CC predisposition to develop a CTGF-associated disorder, and for monitoring
 CC the therapeutic efficacy of treatment of a CTGF-associated disorder, and
 CC also as affinity purification agents. This sequence corresponds to the
 CC anti-human CTGF protein monoclonal antibody light chain protein.
 XX

SQ Sequence 236 AA;

Query Match	96.1%	Score 535;	DB 9;	Length 236;
Best Local Similarity	96.3%	Pred. No. 5.5e-34;		
Matches 103;	Conservative	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1 DIQMTQSPSSASAVDRTVITCRASQISRWLMYQQKEKAPSLIVASSLQGVPs	60		
Db	23 DIQMTQSPSSASAVDRTVITCRASQISRWLMYQQKEKAPSLIVASSLQGVPs	82		
Qy	61 RFSGSGSGTDPFLTISGLQPEDPATYQQVNSYPTFGQGTKVIK	107		
Db	83 RFSGSGSGTDPFLTISLQPBDPATYQQVNSYPTFGQGTKEIK	129		

Search completed: December 3, 2005, 14:25:03
 Job time : 184.992 secs

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OM protein - protein search, using sw model.

Run on: December 3, 2005, 14:11:59 ; Search time 29.2612 Seconds
 (without alignments)

Title: US-10-769-144-8
 Perfect score: 557
 Sequence: 1 DIQMTQSPSSLSASVGDRVTVQWYQQYNSYPRTEGQTKVEIK 107

Scoring table: BL05062 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqB, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$ Maximum Match 100\$

Database : PIR_80;*
 1: PIR1;*
 2: PIR2;*
 3: PIR3;*
 4: PIR4;*

Listing first 45 summaries

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	500	89.8	125	2	S40333		19 kappa chain V-J ant-HIV1 envelope
2	496	89.0	107	2	I69017		19 kappa chain - h
3	491	88.2	129	2	S40369		19 kappa chain V-J
4	489	87.8	131	2	S40352		19 kappa chain V-J
5	486	87.3	117	2	S46376		19 kappa chain - h
6	484	87.1	123	2	S40331		19 kappa chain pre
7	484	86.9	117	2	B21056		19 light chain var
8	483	86.7	128	2	S46372		19 kappa chain V-J
9	480	86.2	117	2	S46371		19 kappa chain V-J
10	480	86.2	125	2	S40353		19 kappa chain pre
11	479	86.0	117	1	K1HUL1		19 kappa chain V-J
12	479	86.0	123	2	S40313		19 kappa chain V-J
13	479	86.0	125	2	S40349		19 kappa chain V-J
14	478	85.8	132	2	S38646		19 kappa chain V-J
15	476	85.5	108	1	K1HUGL		19 kappa chain V-I
16	476	85.5	141	2	A49134		19 kappa chain - h
17	474.5	85.2	107	2	S47183		19 kappa chain V-J
18	474.5	85.2	124	2	S40336		19 kappa chain V-I
19	474	85.1	108	1	K1HUBN		19 kappa chain V-I
20	474	85.1	127	2	S11240		19 kappa chain V-I
21	473	84.9	132	2	S40334		19 kappa chain - h
22	472.5	84.8	107	2	S36275		19 lambda chain V
23	472	84.7	107	2	S36264		19 kappa chain V-I
24	471	84.6	108	2	S49047		19 kappa chain V-I
25	471	84.6	127	2	S40367		19 kappa chain V-I
26	469	84.2	124	2	S40318		19 kappa chain V-I
27	469	84.2	125	2	S40316		19 kappa chain - h
28	468	84.0	108	1	K1HUEU		19 kappa chain V-I
29	467	83.8	108	1	K1HUKU		19 kappa chain V-I

ALIGNMENTS

RESULT 1

S40333
 19 kappa chain V-J region - human
 C;Species: Homo sapiens (man)
 C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C;Accession: S40333
 R;Klein, R.; Jaenichen, R.; Zachau, H. G.
 Bur. J. Immunol. 23:J, 3248-3271, 1993
 A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A;Reference number: S40312; MUID:94080891; PMID:8258341
 A;Status: Preliminary; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-125 <KLE>
 A;Cross-references: UNIPARC:UPI0000116153; EMBL:X72443; PIDN:9441354;
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 F;34-108 Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 500; DB 2; Length 125;
 Best Local Similarity 89.7%; Pred. No. 1.4e-38;
 Matches 96; Conservative 4; Mi smatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTPSPSSLASVYGDRTITCRASQTSRILAWYQQKPEKAKPSLIVASSLQSGVPS 60
 Db 19 DIQMTPSPSSLASVYGDRTITCRASQTSRILAWYQQKPEKAKPSLIVASSLQSGVPS 78

Qy 61 RFSGSGSGTDFLTLSQLOPEDFATTYYCOQYNSYPRTEGQTKVBIK 107
 Db 79 RFSGSGSGTDFLTLSQLOPDFAATTYYCOQYNSYPRWFGGTKVBIK 125

RESULT 2

C;Species: Homo sapiens (man)
 C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
 C;Accession: I69017
 R;Chin, L.T.; Dueñas, M.; Levi, M.; Hinkula, J.; Wahren, B.; Borrebaek, C.A.
 Immunol. Lett. 44, 25-30, 1995
 A;Title: Molecular characterization of a human anti-HIV 1 monoclonal antibody revealed a
 A;Reference number: 154563; MUID:95237884; PMID:721339
 A;Accession: I69017
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-107 <RES>
 A;Cross-references: UNIPARC:UPI0000113F9C; GB:S77140; PIDN:AAB34102.1; PID:
 C;Genetics:

A;Gene: Ig V kappa
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 89.0%; Score 496; DB 2; Length 107;
 Best Local Similarity 90.7%; Pred. No. 2.7e-38;
 Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Db 81 RFSGSGSGTDFSLTSSLOPEDATYYQQNSYPRTEGGTKEIK 127

RESULT 5
 S4376
 Ig kappa chain V-J region (T33-14) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Accession: S4376
 C;Cross-references: UNIPARC:UPI00001165A9; EMBL:227177; PIDN:CAA81701.1; PII:
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin Fc;Domain: immunoglobulin <IMM>

Query Match 89.0%; Score 486; DB 2; Length 117;
 Best Local Similarity 87.9%; Pred. No. 2.4e-37;
 Matches 94; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Db 1 DIQMTQSPSSLSASVGDRVTITCRASQISRLAWYQQKPEAKPSLIYAAASSLQSGVPS 60

Qy 1 DIQMTQSPSSLSASVGDRVTITCRASHDGSYLAWSQKPEAKPSLIYAAASSLQSGVPS 60

Db 1 DIQMTQSPSSLSASVGDRVTITCRASQISRLAWYQQKPEAKPSLIYAAASSLQSGVPS 60

Db 61 RFSGSGSGTDFLTISLQPEDATYYQQNSYPRTEGGTKEIK 107

Db 61 RFSGSGSGTDFLTISLQPEDATYYQQNSYPRTEGGTKEIK 107

A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rea.
 A;Reference number: S46369; MUID:8039491; PMID:94313975;
 A;Accession: 946376
 A;Molecule type: mRNA
 A;Residues: 1-117 <BEN>
 A;Cross-references: UNIPARC:UPI00001165A9; EMBL:227177; PIDN:CAA81701.1; PII:
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin Fc;Domain: immunoglobulin <IMM>

Query Match 87.3%; Score 486; DB 2; Length 117;
 Best Local Similarity 87.9%; Pred. No. 2.4e-37;
 Matches 94; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Db 1 DIQMTQSPSSLSASVGDRVTITCRASQISRLAWYQQKPEAKPSLIYAAASSLQSGVPS 60

Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRLAWYQQKPEAKPSLIYAAASSLQSGVPS 60

Db 10 DIQMTQSPSSLSASVGDRVTITCRASQISRLAWYQQKPEAKPSLIYAAASSLQSGVPS 69

Db 61 RFSGSGSGTDFLTISLQPEDATYYQQNSYPRTEGGTKEIK 107

Db 70 RFSGSGSGTDFLTISLQPEDATYYQQNSYPRTEGGTKEIK 116

RESULT 6
 S4031
 Ig kappa chain - human
 C;Species: Homo sapiens (man)
 C;Accession: S4031
 C;Cross-references: UNIPARC:UPI00001165A9; EMBL:227177; PIDN:CAA81701.1; PII:
 R;Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A;Status: preliminary; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-129 <KLE>
 A;Cross-references: UNIPARC:UPI0000116177; EMBL:X72479; PIDN:9411426; PMID:8258341
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin Fc;Domain: immunoglobulin <IMM>

Query Match 88.2%; Score 491; DB 2; Length 129;
 Best Local Similarity 89.7%; Pred. No. 9.2e-38;
 Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Db 1 DIQMTQSPSSLSASVGDRVTITCRASQISRLAWYQQKPEAKPSLIYAAASSLQSGVPS 60

Db 22 DIQMTQSPSSLSASVGDRVTITCRASHVSNHLYWQQKPEAKPSLIYAAASSLQSGVPS 81

Qy 61 RFSGSGSGTDFLTISLQPEDATYYQQNSYPRTEGGTKEIK 107

Db 82 KFSGSGSGTDFLTISLQPEDATYYQQNSYPRTEGGTKEIK 128

RESULT 7
 S4031
 Ig kappa chain V-J-C region - human
 C;Species: Homo sapiens (man)
 C;Accession: S40352
 C;Cross-references: UNIPARC:UPI0000116166; EMBL:X72462; PIDN:9411392; PMID:CAA51130.1; PII:
 R;Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A;Status: preliminary; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-131 <KLE>
 A;Cross-references: UNIPARC:UPI0000116166; EMBL:X72462; PIDN:9411392; PMID:CAA51130.1; PII:
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin Fc;Domain: immunoglobulin <IMM>

Query Match 87.8%; Score 489; DB 2; Length 131;
 Best Local Similarity 88.8%; Pred. No. 1.4e-37;
 Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Db 1 DIQMTQSPSSLSASVGDRVTITCRASQISRLAWYQQKPEAKPSLIYAAASSLQSGVPS 60

Db 21 DIQMTQSPSSLSASVGDRVTITCRASQISNLAWYQQKPEAKPSLIYAAASSLQSGVPS 80

Qy 61 RFSGSGSGTDFLTISLQPEDATYYQQNSYPRTEGGTKEIK 107

RESULT 7
 B21056
 Ig kappa chain precursor V region (HK134) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Accession: B21056
 C;Cross-references: UNIPARC:UPI0000116166; EMBL:X72462; PIDN:CAA51130.1; PII:
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin Fc;Domain: immunoglobulin <IMM>

Query Match 87.8%; Score 489; DB 2; Length 131;
 Best Local Similarity 88.8%; Pred. No. 1.4e-37;
 Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Db 1 DIQMTQSPSSLSASVGDRVTITCRASQISNLAWYQQKPEAKPSLIYAAASSLQSGVPS 60

Db 21 DIQMTQSPSSLSASVGDRVTITCRASQISNLAWYQQKPEAKPSLIYAAASSLQSGVPS 80

Qy 61 RFSGSGSGTDFLTISLQPEDATYYQQNSYPRTEGGTKEIK 107

R;Bentley, D.L.; Rabbits, T.H.
Cell 32, 181-189, 1983
A;Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicated
A;Reference number: A21056; MUID:83129397; PMID:6402305
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-117 <BEN>
A;Cross-references: UNIPARC:UPI0000116772; GB:K01323; NID:9185995; PIDN:AAA58931.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 86.9%; Score 484; DB 2; Length 117;
Best Local Similarity 97.9%; Pred. No. 3.6e-37;
Matches 93; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
RESULT 8

Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRWLAWYQQKPEKAPSLIYAASSLQSGVPS 60
Db 23 DIQMTQSPSSLSASVGDRVTITCRASQISRWLAWYQQKPEKAPSLIYAASSLQSGVPS 82

Qy 61 RFSGSGSGTDPFLTISGLQPEDFATYYCQQYNNSP 95
Db 83 RFSGSGSGTDPFLTISGLQPEDFATYYCQQYNNSP 117

RESULT 8

S46372
IG light chain variable region (VJ) - human
C;Species: Homo sapiens (man)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S46372
R;Bensimon, C.; Chaetagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rea
A;Reference number: S46365; MUID:94313975; PMID:8039491
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <BEN>
A;Cross-references: UNIPARC:UPI0000176CA4; EMBL:227173
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 86.7%; Score 483; DB 2; Length 128;
Best Local Similarity 89.6%; Pred. No. 4.8e-37;
Matches 95; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
RESULT 8

Qy 2 IOMTQSPSSLSASVGDRVTITCRASQISRWLAWYQQKPEKAPSLIYAASSLQSGVPSR 61
Db 22 IRITQSPSSLSASVGDRVTITCRASQISRWLAWYQQKPEKAPSLIYAASSLQSGVPSR 81

Qy 62 FSGSGSGTDPFLTISGLQPEDFATYYCQQYNNSPRTFGQTKVEIK 107
Db 82 FSGSGSGTDPFLTISGLQPEDFATYYCQQYNNSPRTFGQTKVEIK 127

RESULT 8

S46371
19 kappa chain V-J region (T24-3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 01-SEP-1995 #text_change 21-Jan-2000
C;Accession: S46371; S38645
R;Bensimon, C.; Chaetagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rea
A;Reference number: S46369; MUID:94313975; PMID:8039491

RESULT 9

S46371
19 kappa chain V-J region (T24-3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 01-SEP-1995 #text_change 21-Jan-2000
C;Accession: S46371; S38645
R;Bentley, D.L.; Rabbits, T.H.
Cell 32, 181-189, 1983
Nature 288, 730-733, 1980
A;Title: Human immunoglobulin V genes: evidence indicating that recently duplicat
A;Reference number: A21056; MUID:83129397; PMID:6402305
A;Accession: A01881; MUID:81098966; PMID:6779204
A;Molecule type: DNA
A;Residues: 1-117 <BEN1>
A;Cross-references: UNIPROT:P01601; UNIPARC:UPI000012E44; GB:V00558; GB:J00244; GB:J002
A;Note: the sequence was determined from the germline gene
R;Bentley, D.L.; Rabbits, T.H.
Cell 32, 181-189, 1983
A;Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicat
A;Reference number: A21056; MUID:83129397; PMID:6402305
A;Accession: A21056
A;Molecule type: DNA
A;Residues: 1-117 <BEN2>
A;Cross-references: UNIPARC:UPI000012E44; GB:K01322; NID:9415959; PIDN:CAA81696.1; PID
C;Genetics:
A;Gene: GDB:IGKV1

C;Keywords: heterotrimer; immunoglobulin
F;23-97/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 480; DB 2; Length 117;
Best Local Similarity 85.3%; Pred. No. 8.3e-37;
Matches 93; Conservative 7; Mismatches 2; Indels 2; Gaps 1;
Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRWLAWYQQKPEKAPSLIYAASSLQSGVPS 60
Db 8 DIQMTQSPSSLSASVGDRVTITCRASQISRWLAWYQQKPEKAPSLIYAASSLQSGVPS 67
Qy 61 RFSGSGSGTDPFLTISGLQPEDFATYYCQQYNNSY-PRTFGQTKVEIK 107
Db 68 RFSGSGSGTDPFLTISGLQPEDFATYYCQQYNNSYFPPTFGQTKVEIK 116

RESULT 10

S40353
Ig kappa chain V-J-C region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40353
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:9408091; PMID:8258341
A;Accession: S40353
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <KLE>
A;Cross-references: UNIPARC:UPI00000176CAE; EMBL:X72463
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;30-104/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 480; DB 2; Length 125;
Best Local Similarity 87.9%; Pred. No. 8.9e-37;
Matches 94; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
RESULT 11

Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRWLAWYQQKPEKAPSLIYAASSLQSGVPS 60
Db 15 DIQMTQSPSSLSASVGDRVTITCRASQISRWLAWYQQKPEKAPSLIYAASSLQSGVPS 74
Qy 61 RFSGSGSGTDPFLTISGLQPEDFATYYCQQYNNSYFPPTFGQTKVEIK 107
Db 75 RFSGSGSGTDPFLTISGLQPEDFATYYCQQYNNSYFPPTFGQTKVEIK 121

A;Title: Human immunoglobulin variable region genes - DNA sequences of two V-kappa genes
A;Reference number: A93241; MUID:81098966; PMID:6779204
A;Accession: A01881
A;Molecule type: DNA
A;Residues: 1-117 <BEN1>
A;Cross-references: UNIPROT:P01601; UNIPARC:UPI000012E44; GB:V00558; GB:J00244; GB:J002
A;Note: the sequence was determined from the germline gene
R;Bentley, D.L.; Rabbits, T.H.
Cell 32, 181-189, 1983
A;Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicat
A;Reference number: A21056; MUID:83129397; PMID:6402305
A;Accession: A21056
A;Molecule type: DNA
A;Residues: 1-117 <BEN2>
A;Cross-references: UNIPARC:UPI000012E44; GB:K01322; NID:9415959; PIDN:CAA81696.1; PID
C;Genetics:
A;Gene: GDB:IGKV1

A; Cross-references: GDB:136264
 A; Map position: 2p12-2p12
 A; Introns: 19/1
 C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (Ig) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
 C; Superfamily: immunoglobulin V region; immunoglobulin homology
 C; Keywords: heterotetramer
 F; 1-22 /Domain: signal sequence #status predicted <SIG>
 F; 23-112 /Domain: Ig kappa chain V-I region (HK1) #status predicted <IMM>
 F; 112-112 /Domain: immunoglobulin homology <IMM>
 F; 45-110 /Disulfide bonds: #status predicted

Query Match Score 479; DB 1; Length 117;
 Best Local Similarity 96.8%; Pred. No. 1e-36;
 Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTOQSPSSLNASVGDRVTITCRASQGSRMLWYQQPKPAPKSLIVAAASSLQSGVFS 60
 Db 23 DIQMTOQSPSSLNASVGDRVTITCRASQGSRMLWYQQPKPAPKSLIVAAASSLQSGVFS 82

Qy 61 RFSGSGSGTDTFLTISGLQPEDPATYQQYNNSYP 95
 Db 83 RFSGSGSGTDTFLTISLQPEDPATYQQYNNSYP 117

RESULT 12
 S40313 Ig kappa chain V-J region - human
 C; Species: Homo sapiens (man)
 C; Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C; Accession: S40313
 R; Klein, R.; Jaenichen, R.; Zachau, H.G.
 A; Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A; Reference number: S40312; MUID:94080891; PMID:8258341
 A; Status: preliminary; translation not shown
 A; Molecule type: mRNA
 A; Residues: 1-123 <KLE>
 A; Cross-references: UNIPARC:UPI000011613F; EMBL:X72423; NID:9411314; PIDN:CAA51091.1; PI
 C; Superfamily: immunoglobulin V region; immunoglobulin homology
 C; Keywords: heterotetramer; immunoglobulin
 F; 132-106 /Domain: immunoglobulin homology <IMM>

Query Match Score 479; DB 2; Length 123;
 Best Local Similarity 87.9%; Pred. No. 1.e-36;
 Matches 94; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTOQSPSSLNASVGDRVTITCRASQGSRMLWYQQPKPAPKSLIVAAASSLQSGVFS 60
 Db 17 DIQMTOQSPSSLNASVGDRVTITCRASQGSRMLWYQQPKPAPKSLIVAAASSLQSGVFS 76

Qy 61 RFSGSGSGTDTFLTISGLQPEDPATYQQYNNSYPRTFGQGTVEIK 107
 Db 77 RFSGSGSGTDTFLTISLQPEDPATYCLQNGYDRTFGQGTVEIK 123

RESULT 13
 S40349 Ig kappa chain V-J region - human
 C; Species: Homo sapiens (man)
 C; Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 C; Accession: S40349
 R; Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A; Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A; Reference number: S40312; MUID:94080891; PMID:8258341
 A; Status: preliminary; translation not shown
 A; Molecule type: mRNA
 A; Residues: 1-125 <KLE>
 A; Cross-references: UNIPARC:UPI0000116163; EMBL:X72459; NID:9411386; PIDN:CAA51127.1; PI
 C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotetramer; immunoglobulin
 F; 33-107 /Domain: immunoglobulin homology <IMM>

Query Match Score 479; DB 2; Length 125;
 Best Local Similarity 88.7%; Pred. No. 1.e-36;
 Matches 94; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 2 IOMTQSPSSLNASVGDRVTITCRASQGSRMLWYQQPKPAPKSLIVAAASSLQSGVFS 61
 Db 19 IOMTQSPSSLNASVGDRVTITCRASQGSSLAWYQQPKPAPKLLYDASSLQSGVFS 78

Qy 62 FGSGSGTDTFLTISGLQPEDPATYQQYNNSYPRTFGQGTVEIK 107
 Db 79 FGSGSGTDTFLTISLQPEDPATYQQFNTPYPLTFRGGTVEIK 124

RESULT 14
 S38646 Ig kappa chain V region - human (fragment)
 C; Species: Homo sapiens (man)
 C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C; Accession: S38646
 R; Bensimon, C.; Chastagner, P.; Zouani, M.
 A; Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
 A; Reference number: S38643
 A; Accession: S38646
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-132 <BEN>
 A; Cross-references: UNIPARC:UPI00001165A5; EMBL:Z27173; NID:g415961; PIDN:CAA81697.1; PI
 C; Superfamily: immunoglobulin V region; immunoglobulin homology
 C; Keywords: heterotetramer; immunoglobulin
 F; 40-114 /Domain: immunoglobulin homology <IMM>

Query Match Score 478; DB 2; Length 132;
 Best Local Similarity 88.7%; Pred. No. 1.e-36;
 Matches 94; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 2 IOMTQSPSSLNASVGDRVTITCRASQGSRMLWYQQPKPAPKSLIVAAASSLQSGVFS 61
 Db 26 IRIAQSPSSLUSTDRTVTITCRASQGSSLYAWYQQPKPAPKLLYAASTLQSGVFS 85

Qy 62 FGSGSGTDTFLTISGLQPEDPATYQQYNNSYPRTFGQGTVEIK 107
 Db 86 FGSGSGTDTFLTISCLOSEDFATYQQYSYPRTFQGTVEIK 131

RESULT 15
 K1HUGL Ig kappa chain V-I region (Gal) - human (tentative sequence)
 C; Species: Homo sapiens (man)
 C; Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
 C; Accession: A01867
 R; Laure, C.J.; Watanabe, S.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 354, 1503-1504, 1973
 A; Title: The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal), 1
 A; Reference number: A01867
 A; Accession: A01867
 A; Molecule type: protein
 A; Residues: 1-108 <LAU>
 A; Cross-references: UNIPROT:P01599; UNIPARC:UPI000012E142
 A; Note: The C region of this chain has the Inv (3) marker
 C; Comment: This chain was isolated from a Waldenstrom's macroglobulin.
 C; Genetics:
 A; Gene: GDB:IGKV1
 A; Cross-references: GDB:136264
 A; Map Position: 2p12-2p12
 C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (Kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
 C; Superfamily: immunoglobulin V region; immunoglobulin homology
 C; Keywords: heterotetramer

F:23-88/Disulfide bonds: #status predicted
Query Match 85.5%; Score 476; DB 1; Length 108;
Best Local Similarity 86.9%; Pred. No. 1.8e-36;
Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRWLAWYQQPEKAPSLIVYASSILOSSGPS 60
Db 1 DIQMTQSPSSLSASVGDRVTITCRASQIRNDLTWQQPKPKAPKELIVYASNLLOSSGPS 60
Qy 61 RFSGSGSGTDFLTISGLQPEDFATYQQYNSYPRTFGQCTKVEIK 107
Db 61 RFSGSGAGTEFLTISLQPEDFATYCLQQNSYPRSFQGCTKVEIK 107

Search completed: December 3, 2005, 14:33:32
Job time : 29.2612 sec

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Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	28	491	88.2	109	2	US-09-490-324-28
OM protein - protein search, using sw model		29	491	88.2	109	2	US-09-490-324-43
Run on:	December 3, 2005, 13:24:58 ; Search time 45.4204 Seconds (without alignments)	30	488	87.6	108	2	US-08-1974-899-2
Title:	US-10-769-144-8	31	488	87.6	108	2	US-09-795-198-2
Perfect score:	557	32	486	87.3	107	2	US-10-330-613A-1B
Sequence:	1 DIQMTQSPSSLSASVGDRVTI...CQQYNSYPRTFGQTKVEIK 107	33	484	86.9	107	2	US-08-1599-226-1
Scoring table:	BLOSUM62	34	484	86.9	107	2	US-09-125-098-1
Gapop:	10.0 , Gapext 0.5	35	484	86.9	107	2	US-09-1540-188-1
Searched:	572060 seqs, 82675679 residues	36	484	86.9	117	2	US-09-042-353-18
Total number of hits satisfying chosen parameters:	572060	37	484	86.9	117	2	US-08-758-417A-313
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Maximum DB seq length: 2000000000		39	483	86.7	107	2	US-09-125-098-9
Post-processing: Minimum Match 0%		40	483	86.7	107	2	US-09-540-018-9
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Listing first 45 summaries		42	481.5	86.4	109	2	US-09-798-558-4
Database :	Issued Patents AA:*	43	481	86.4	107	1	US-08-276-852-84
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	2: /cgn2_6/prodata/1/iaa/6_COMB_pep:*	45	481	86.4	107	1	US-08-899-575-84
	3: /cgn2_6/prodata/1/iaa/H_COMB_pep:*						
	4: /cgn2_6/prodata/1/iaa/PCTRS_COMB_pep:*						
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Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
	SUMMARIES						
Result No.	Query	Match Length	DB ID	Description			
1	529	95.0	108	2 US-09-920-262A-8	Sequence 8, Appli		
2	499	89.6	107	1 US-07-334-373C-18	Sequence 18, Appli		
3	499	89.6	107	2 US-08-337-642B-18	Sequence 18, Appli		
4	499	89.6	107	2 US-08-146-205C-18	Sequence 18, Appli		
5	499	89.6	107	2 US-09-648-067A-14	Sequence 14, Appli		
6	499	89.6	107	2 US-09-705-686-18	Sequence 18, Appli		
7	499	89.6	107	2 US-09-705-392A-18	Sequence 18, Appli		
8	499	89.6	107	2 US-09-705-398-18	Sequence 18, Appli		
9	499	89.6	107	2 US-09-602-812A-5	Sequence 5, Appli		
10	499	89.6	107	4 PCT-US93-07832-18	Sequence 18, Appli		
11	499	89.6	108	2 US-08-146-206C-3	Sequence 3, Appli		
12	499	89.6	108	2 US-09-795-798-3	Sequence 3, Appli		
13	499	89.6	108	2 US-09-908-469-12	Sequence 12, Appli		
14	497	89.2	109	1 US-07-934-373C-3	Sequence 3, Appli		
15	497	89.2	109	2 US-08-337-642B-3	Sequence 3, Appli		
16	497	89.2	109	2 US-08-146-206C-3	Sequence 3, Appli		
17	497	89.2	109	2 US-09-705-686-3	Sequence 3, Appli		
18	497	89.2	109	2 US-09-705-392A-3	Sequence 3, Appli		
19	497	89.2	109	2 US-09-705-398-3	Sequence 3, Appli		
20	497	89.2	109	4 PCT-US93-07832-3	Sequence 3, Appli		
21	497	89.2	236	2 US-09-859-052-30	Sequence 30, Appli		
22	497	88.2	109	2 US-09-055-763B-28	Sequence 43, Appli		
23	491	88.2	109	2 US-09-055-763B-43	Sequence 43, Appli		
24	491	88.2	109	2 US-09-190-070A-28	Sequence 28, Appli		
25	491	88.2	109	2 US-09-410-070A-43	Sequence 43, Appli		
26	491	88.2	109	2 US-09-410-153-28	Sequence 28, Appli		
27	491	88.2	109	2 US-09-410-153-43	Sequence 43, Appli		
	ALIGMENTS						
RESULT 1							
	US-09-920-262A-8						
	; Sequence 8, Application US/09920262A						
	; Patent No. 6902734						
	GENERAL INFORMATION:						
	; APPLICANT: Shealy, David						
	; Knight, David						
	; Scalzon, Bernie						
	; Giles-Komar, Jill						
	; APPLICANT: Peritt, David						
	; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES						
	; FILE REFERENCE: CEN048						
	CURRENT APPLICATION NUMBER: US/09/920,262A						
	PRIOR APPLICATION NUMBER: 2002-05-06						
	PRIOR FILING DATE: 2002-05-07						
	PRIOR FILING DATE: 2000-09-29						
	NUMBER OF SEQ ID NOS: 15						
	SOFTWARE: PatentIn Ver 3.1						
	SEQ ID NO: 8						
	LENGTH: 108						
	; TYPE: PRT						
	; ORGANISM: Homo sapiens						
	US-09-920-262A-8						
	Query Match	95	0%	Score 529;	DB 2;	Length 108;	
	Best Local Similarity	95	0%	Pred. No. 1.8-44;			
	Matches 102; Conservative	1	Mismatches	Indels 0;			
	Qy	1 DIQMTQSPSSLSASGDRVITCRASQISWLNQKPEKAPSLIYASSLQGVPS	60	Db	1 DIQMTQSPSSLSASGDRVITCRASQISWLNQKPEKAPSLIYASSLQGVPS	60	
	Qy	61 RFSGSGSGTGTDTLTISLQPEDFATYCQOINIVPTFGQTKBLIK	107	Db	61 RFSGSGSGTGTDTLTISLQPEDFATYCQOINIVPTFGQTKBLIK	107	
	RESULT 2						
	US-07-934-373C-18						
	; Sequence 18, Application US/07934373C						
	; Patent No. 581337						
	GENERAL INFORMATION:						
	; APPLICANT: Paul J. Carter						
	; APPLICANT: Leonard G. Presta						
	TITLE OF INVENTION: Immunoglobulin Variant						
	; NUMBER OF SEQUENCES: 48						
	CORRESPONDENCE ADDRESS:						
	ADDRESSEE: Genentech, Inc.						

STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/934,373C
 FILING DATE: 21-Aug-1992
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/05126
 FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/715272
 FILING DATE: 14-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 FILING DATE: 14-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P0709P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/925-1994
 FAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-07-934-373C-18

Query Match 89.6%; Score 499; DB 2; Length 107;
 Best Local Similarity 91.6%; Pred. No. 1.5e-41;
 Matches 98; Conservative 2; Missmatches 7; Indels 0;
 Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQGISRMLAWYQQKPEKAPKSLIYAAASSLQSGVPS 60
 Db 1 DIQMTQSPSSLSASVGDRVTITCRASQISNYLAWYQQKPEKAPKSLIYAAASSLQSGVPS 60

Qy 61 RFGSGSGGTDFTLTSGLOPEDFATYYQQNSYPRTFGGTKEIK 107
 Db 61 RFGSGSGGTDFTLTSSLQPEDFATYYQQNSLPWTFGGTKEIK 107

RESULT 3
 US-08-437-642B-18
 Patient No. 6054297

GENERAL INFORMATION:
 APPLICANT: Paul J. Carter
 TITLE OF INVENTION: Immunoglobulin Variants
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/437,642B
 FILING DATE: 09-May-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/934373
 FILING DATE: 21-AUG-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/146206
 FILING DATE: 17-NOV-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/05126
 FILING DATE: 15-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/715272
 FILING DATE: 14-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P0709P2C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/925-1994
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-437-642B-18

Query Match 89.6%; Score 499; DB 2; Length 107;
 Best Local Similarity 91.6%; Pred. No. 1.5e-41;
 Matches 98; Conservative 2; Missmatches 7; Indels 0;
 Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQGISRMLAWYQQKPEKAPKSLIYAAASSLQSGVPS 60
 Db 1 DIQMTQSPSSLSASVGDRVTITCRASQISNYLAWYQQKPEKAPKSLIYAAASSLQSGVPS 60

Qy 61 RFGSGSGGTDFTLTSGLOPEDFATYYQQNSYPRTFGGTKEIK 107
 Db 61 RFGSGSGGTDFTLTSSLQPEDFATYYQQNSLPWTFGGTKEIK 107

RESULT 4
 US-08-437-642B-18
 Sequence 18, Application US/08146206C
 Patent No. 6407213

GENERAL INFORMATION:
 APPLICANT: Carter, Paul J.
 APPLICANT: Presta, Leonard G.
 TITLE OF INVENTION: Method For Making Humanized Antibodies
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/146,206C
 FILING DATE: 17-No. 6407213-1993
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/715272
 FILING DATE: 14-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P0709P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/925-1994
 TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-146-206C-18

Query Match : Score 89.6%; Pred. No. 1.5e-41; Length 107;
 Best Local Similarity 91.6%; Indels 0; Gaps 0;
 Matches 98; Conservative 2; Mismatches 7;

Qy	1 DIQMTQSPSSLASVGDRVTITCRASQISRMWYQQKPEKAQPKSLIYAAASSLQSGVPS 60
Db	1 DIQMTQSPSSLASVGDRVTITCRASQISNYLAWQQPKSKAPKLIYAAASSLQSGVPS 60

Qy 61 RFGSGSGTDFLTITSSQPEDFATYYCQQQNSYPRTFGQGTKEIK 107
 Db 61 RFGSGSGTDFLTITSSQPEDFATYYCQQINSLPWTFGQGTKEIK 107

RESULT 5

US-09-648-067A-14

Sequence 14, Application US/09648067A

Patent No. 662196

GENERAL INFORMATION:

APPLICANT: Baughn, Sharon A.

APPLICANT: Shak Steven

TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies

FILE REFERENCE: P1775RI

CURRENT APPLICATION NUMBER: US/09/648,067A

CURRENT FILING DATE: 2000-08-25

PRIOR APPLICATION NUMBER: US 60/151,018

PRIOR FILING DATE: 1999-08-27

PRIOR APPLICATION NUMBER: US 60/213,822

PRIOR FILING DATE: 2000-06-23

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 14

TYPE: PRT

ORGANISM: Artificial sequence

OTHER INFORMATION: VL consensus sequence

US-09-648-067A-14

Query Match : Score 89.6%; Pred. No. 1.5e-41; Length 107;
 Best Local Similarity 91.6%; Indels 0; Gaps 0;

Matches 98; Conservative 2; Mismatches 7;

Qy	1 DIQMTQSPSSLASVGDRVTITCRASQISRMWYQQKPEKAQPKSLIYAAASSLQSGVPS 60
Db	1 DIQMTQSPSSLASVGDRVTITCRASQISNYLAWQQPKSKAPKLIYAAASSLQSGVPS 60

Qy 61 RFGSGSGTDFLTITSSQPEDFATYYCQQQNSYPRTFGQGTKEIK 107

Db 61 RFGSGSGTDFLTITSSQPEDFATYYCQQINSLPWTFGQGTKEIK 107

RESULT 7

US-09-705-392A-18

Sequence 18, Application US/09705392A

Patent No. 6719971

GENERAL INFORMATION:

APPLICANT: Carter, Paul J.

PRESTA, LEONARD G.

TITLE OF INVENTION: Method For Making Humanized Antibodies

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 02-No. 663955-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/146206

FILING DATE: 17-NOV-1993

APPLICATION NUMBER: 07/715272

FILING DATE: 14-JUN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 PRIORITY/DOCKET NUMBER: P0709P1D1 REVISED
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1994
 FAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 18;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 18:
 US-09-705-392A-18

Query Match 89.6%; Score 499; DB 2; Length 107;
 Best Local Similarity 91.6%; Pred. No. 1.5e-41;
 Matches 98; Conservative 2; Mismatches 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRSRMLAWYQQKPEKAPSKLIVASSLGSVPS 60
 Db 1 DIQMTQSPSSLSASVGDRVTITCRASQISRSRMLAWYQQKPEKAPSKLIVASSLGSVPS 60

Qy 61 RFSGSGSGTDFLTISGLOPEDFATYCOOYNNSYRTFGQGTKVBIK 107
 Db 61 RFSGSGSGTDFLTISGLOPEDFATYCOOYNNSLWTFCGGTKVBIK 107

RESULT 8
 US-09-705-398-18
 Sequence 18, Application US/09705398
 Patent No. 6800738
 GENERAL INFORMATION:
 APPLICANT: Carter, Paul J.
 PRESTA, Leonard G.
 TITLE OF INVENTION: Method for Making Humanized Antibodies
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/705-398
 FILING DATE: 02-NO-6800738-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/146206
 FILING DATE: 17-NOV-1993
 APPLICATION NUMBER: 07/715272
 FILING DATE: 14-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 PRIORITY/DOCKET NUMBER: P0709P1D2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1994
 FAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 18;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 18:
 US-09-705-398-18

Query Match 89.6%; Score 499; DB 2; Length 107;

Best Local Similarity 91.6%; Pred. No. 1.5e-41;
 Matches 98; Conservative 2; Mismatches 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRSRMLAWYQQKPEKAPSKLIVASSLGSVPS 60
 Db 1 DIQMTQSPSSLSASVGDRVTITCRASQISRSRMLAWYQQKPEKAPSKLIVASSLGSVPS 60

Qy 61 RFSGSGSGTDFLTISGLOPEDFATYCOOYNNSYRTFGQGTKVBIK 107
 Db 61 RFSGSGSGTDFLTISGLOPEDFATYCOOYNNSLWTFCGGTKVBIK 107

RESULT 9
 US-09-602-812A-5
 Sequence 5, Application US/09602812A
 Patent No. 6949215
 GENERAL INFORMATION:
 APPLICANT: Adams, Camellia W.
 PRESTA, Leonard G.
 SILIWOWSKI, Mark X.
 TITLE OF INVENTION: Humanized Anti-Brb2 Antibodies and Treatment with
 HUMANIZED ANTI-BRB2 ANTIBODIES
 CURRENT APPLICATION NUMBER: US/09/602,812A
 CURRENT FILING DATE: 2000-06-23
 PRIORITY APPLICATION NUMBER: US 60/141,316
 PRIORITY FILING DATE: 1999-06-25
 NUMBER OF SEQ ID NOS: 13
 SEQ ID NO 5
 LENGTH: 107
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: Light chain consensus sequence
 US-09-602-812A-5

Query Match 89.6%; Score 499; DB 2; Length 107;
 Best Local Similarity 91.6%; Pred. No. 1.5e-41;
 Matches 98; Conservative 2; Mismatches 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQISRSRMLAWYQQKPEKAPSKLIVASSLGSVPS 60
 Db 1 DIQMTQSPSSLSASVGDRVTITCRASQISRSRMLAWYQQKPEKAPSKLIVASSLGSVPS 60

Qy 61 RFSGSGSGTDFLTISGLOPEDFATYCOOYNNSYRTFGQGTKVBIK 107
 Db 61 RFSGSGSGTDFLTISGLOPEDFATYCOOYNNSLWTFCGGTKVBIK 107

RESULT 10
 PCT-US93-07832-18
 Sequence 18, Application PC/TUS9307832
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc.
 TITLE OF INVENTION: Immunoglobulin Variants
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 07-15272
 FILING DATE: 17-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 PRIORITY/DOCKET NUMBER: P0709P1D2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1994
 FAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 18;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 18:
 US-09-705-398-18

Query Match 89.6%; Score 499; DB 2; Length 107;

APPLICATION NUMBER: 07/715272
 FILING DATE: 14-JUN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/05126
 FILING DATE: 15-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/934373
 FILING DATE: 21-AUG-1992
 ATTORNEY/AGENT INFORMATION:
 NAME:
 REGISTRATION NUMBER:
 REFERENCE/DOCKET NUMBER: 709P2PCT
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 415/952-9881
 TELEX: 910/371-2168
 INFORMATION FOR SEQ ID NO: 1B:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 PCR-US93-07832-18

Query Match 89.6%; Score 499; DB 4; Length 107;
 Best Local Similarity 91.6%; Pred. No. 1.5e-41;
 Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Query Match 89.6%; Score 499; DB 2; Length 108;
 Best Local Similarity 91.6%; Pred. No. 1.5e-41;
 Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

RESULT 11
 US-08-974-899-3
 Sequence 3, Application US/08974899
 GENERAL INFORMATION:
 Patent No. 6037454
 APPLICANT: Presta, Leonard G.
 APPLICANT: Jardieu, Paula M.
 TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESS: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/795,798
 FILING DATE: 28-Feb-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/974,899
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P1014R1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1994
 TELEFAX: 650/982-9881
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 108 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-08-974-899-3

RESULT 12
 US-09-795-798-3
 Sequence 3, Application US/09795798
 GENERAL INFORMATION:
 Patent No. 6703018
 APPLICANT: Presta, Leonard G.
 APPLICANT: Jardieu, Paula M.
 TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESS: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: FC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/795,798
 FILING DATE: 28-Feb-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/974,899
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P1014R1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1994
 TELEFAX: 650/982-9881
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 108 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-795-798-3

Query Match 89.6%; Score 499; DB 2; Length 108;
 Best Local Similarity 91.6%; Pred. No. 1.5e-41;
 Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Query Match 89.6%; Score 499; DB 2; Length 107;
 Best Local Similarity 91.6%; Pred. No. 1.5e-41;
 Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

RESULT 13
 US-09-795-798-3
 Sequence 3, Application US/09795798
 GENERAL INFORMATION:
 Patent No. 6703018
 APPLICANT: Presta, Leonard G.
 APPLICANT: Jardieu, Paula M.
 TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESS: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,899
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P1014R1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1994
 TELEFAX: 650/982-9881
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 108 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-795-798-3

Query Match 89.6%; Score 499; DB 2; Length 107;
 Best Local Similarity 91.6%; Pred. No. 1.5e-41;
 Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Query Match 89.6%; Score 499; DB 2; Length 107;
 Best Local Similarity 91.6%; Pred. No. 1.5e-41;
 Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

RESULT 13
US-08-908-469-12
Sequence 12, Application US/08908469
Patent No. 6884879

GENERAL INFORMATION:

APPLICANT: Bacca, Manuel
Wellis, James A.
Presta, Leonard G.
Lowman, Henry B.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908,469

FILING DATE: 21-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/833,504

FILING DATE: 07-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-08-908-469-12

Query Match Score 89.6%; Length 108;

Best Local Similarity 91.6%; Pred. No. 1.5e-41;

Matches 2; Mismatches 7; Indels 0; Gaps 0;

RESULT 14
US-07-934-373C-3
Sequence 3, Application US/07934373C
Patent No. 5811337

GENERAL INFORMATION:

APPLICANT: Paul J. Carter

APPLICANT: Leonard G. Presta

TITLE OF INVENTION: Immunoglobulin Variants

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSEES: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

FILING DATE: 09-May-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/934373

FILING DATE: 21-AUG-1992

STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/934,373C

FILING DATE: 21-Aug-1992

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/05126

FILING DATE: 15-JUN-1992

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 07/152272

FILING DATE: 14-JUN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P0709P2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1994

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-07-934-373C-3

Query Match Score 89.2%; Score 497; DB 1; Length 109;

Best Local Similarity 90.7%; Pred. No. 2.4e-41;

Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

RESULT 15
US-08-437-642B-3
Sequence 3, Application US/08437642B

Patent No. 6054277

GENERAL INFORMATION:

APPLICANT: Paul J. Carter

APPLICANT: Leonard G. Presta

TITLE OF INVENTION: Immunoglobulin Variants

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEES: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

FILING DATE: 09-May-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/437,642B

FILING DATE: 21-AUG-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Le, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-3

Query Match 89.2%; Score 497; DB 2; Length 109;
Best Local Similarity 90.7%; Pred. No. 2.4e-41;
Matches 97; Conservative 3; Mismatches -7; Indels 0; Gaps 0;

Qy 1 DIQMTOSSPSLSSASVGDRTVTITCRASQIGSRWLAVYQQREKEAPSLIVIAASSLQSGVPS 60
Db 1 DIQMTOSSPSLSSASVGDRTVTITCRASQDVSSYLAVYQQKGKAPKLIVIAASSLQSGVPS 60

Qy 61 RFGSGSGSGTDPDTLTISGLQPEDPATYCCQYNSYPRTEGGTKEIK 107
Db 61 RFSGSGSGTDPDTLTISLQPEDPATYCCQYNSLPYTFGQGTKVBIK 107

Search completed: December 3, 2005, 14:11:29
Job time : 46.4204 sec

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 3, 2005, 13:24:58 ; Search time 49.2408 Seconds
 (without alignments)
 194.765 Million cell updates/sec

Title: US-10-769-144-4

Perfect score: 621

Sequence: 1 EVQLVQSAEVKPKGSLRIL...TRGDRGVYWGQTLVTVSS 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqB, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : Issued Patents AA:
 1: /cgn2_6/pctdata/1/iaa5_COMB.pep:/*
 2: /cgn2_6/pctdata/1/iaa6_COMB.pep:/*
 3: /cgn2_6/pctdata/1/iaaH_COMB.pep:/*
 4: /cgn2_6/pctdata/1/iaa_PCTUS_COMB.pep:/*
 5: /cgn2_6/pctdata/1/iaaRE_COMB.pep:/*
 6: /cgn2_6/pctdata/1/iaa/backfiles1.pep:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query ID	Score	Match	Length	Description
1	556	89.5	120	2	US-09-025-769B-40
2	556	89.5	120	2	US-09-025-769B-67
3	556	89.5	120	2	US-09-090-070A-40
4	556	89.5	120	2	US-09-090-070A-67
5	556	89.5	120	2	US-09-090-153-40
6	556	89.5	120	2	US-09-090-153-67
7	556	89.5	120	2	US-09-090-324-40
8	553	89.1	119	2	US-09-025-769B-26
9	553	89.1	119	2	US-09-090-153-26
10	553	89.1	119	2	US-09-090-153-26
11	553	89.1	119	2	US-09-090-153-26
12	553	89.1	119	2	US-09-090-324-26
13	496.5	80.5	119	2	US-09-090-262A-7
14	496.5	80.0	129	1	US-08-665-202-32
15	496.5	80.0	129	2	US-09-315-573-32
16	496.5	80.0	258	2	US-08-665-202-5
17	496.5	80.0	258	2	US-09-335-574-5
18	496.5	80.0	262	2	US-09-099-821-4
19	496.5	80.0	262	2	US-09-956-087-4
20	496.5	80.0	282	2	US-09-920-592A-7
21	496.5	80.0	282	2	US-09-985-442-7
22	496.5	80.0	282	2	US-09-933-580-7
23	495	79.7	98	1	US-08-665-202-33
24	495	79.7	98	2	US-09-315-573-33
25	495	79.7	98	2	US-10-194-975-45
26	495	79.7	98	2	US-08-545-809A-133
27	495	79.7	117	2	US-09-025-769B-40

ALIGNMENTS

RESULT 1
 US-09-025-769B-40
 ; Sequence 40, Application US/09025769B
 ; Patent No. 6300064

GENERAL INFORMATION:

APPLICANT: Knapik, Achim
 APPLICANT: Pack, Peter
 APPLICANT: Iliaq, Vic
 APPLICANT: Ge, Liming
 APPLICANT: Moroney, Simon
 APPLICANT: Plueckhun, Andreas
 TITLE OF INVENTION: Protein/(Poly)peptide libraries
 NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0., Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B
 FILING DATE: 18-PB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9090
 TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein

Query Match Score 556; DB 2; Length 120;
 Best Local Similarity 89.2%; Pred. No. 1e-48;
 Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

Qy 1 EVQLVSGAELYKPGESLIRSKGSQSDSFITYWIGVRMPGKGLEMGGIYPGDSDTY 60
 Db 1 EVQLVSGAELYKPGESLIRSKGSQSDSFITYWIGVRMPGKGLEMGGIYPGDSDTY 60
 Qy 61 SPSFQQVTISADKSISTAYLQSSLKASDAMYCTR --- GDRGVDTWQGTLTVSS 116
 Db 61 SPSFQQVTISADKSISTAYLQSSLKASDAMYCTR --- GDRGVDTWQGTLTVSS 120

RESULT 2

US 09-025-769B-67
 Sequence 67, Application US/09025769B

GENERAL INFORMATION:

Patent No. 6300064

APPLICANT: Knappik, Achim

Pack, Peter

Illeg, Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly) peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: Colin G. Sanderson, Esq. c/o Heller Ehrman

White & McAuliffe

Street: 1666 K Street, N.W., Suite 300

City: Washington

State: D.C.

Country: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sanderson, Esq.

REGISTRATION NUMBER: 311298

REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: Protein

SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-09-490-070A-40

Query Match 89 5%; Score 556; DB 2; Length 120;

Best Local Similarity 89 2%; Pred. No. 1e-48; Gaps 1;

Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

RESULT 4

US 09-490-070A-67

Sequence 67, Application US/09490070A

Patent No. 6696248

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Illeg, Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly) peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: Colin G. Sanderson, Esq. c/o Heller Ehrman

RESULT 3

US 09-490-070A-40

Sequence 40, Application US/09490070A

Patent No. 6696248

STREET: White & McAuliffe, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20006

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/490,070A
 FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Colin G. Sandercock, Esq.
 REGISTRATION NUMBER: 31,298
 REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 912-2000
 TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 67:
 US-09-490-070A-67

Query Match 89.5%; Score 556; DB 2; Length 120;
 Best Local Similarity 89.2%; Pred. No. 1e-48;
 Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

RESULT 6
 US-09-490-153-67

Qy 1 EVQLVQSAEVVKPGESLRISCKSGSDFTYWMQPKGLEMMGIIYPGDSDTIY 60
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1 EVQLVQSAEVVKPGESTKISCKSGSYFTSYWGMQPKGLEMMGIIYPGDSDTIY 60

Qy 61 SPSRFQQTISADKSISSTAYLQSSLKASDAMYCCTR---GDRGVYDYMGGTLYTVSS 116
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 61 SPSRFQQTISADKSISSTAYLQSSLKASDAMYCCTR---GDRGVYDYMGGTLYTVSS 116

RESULT 5
 US-09-490-153-40

Qy Sequence 40, Application US/09490153
 Patent No. 6706484

GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pack, Peter
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Plueckthun, Andreas

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:
 James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/490,153

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 TELEFAX: (212) 596-9090
 INFORMATION FOR SEQ ID NO: 67:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID N
 S-09-490-153-67

Query Match	89 5%	Score
Best Local Similarity	89 2%	Pred.
Matches 107;	Conservative	3; Mi
b	1 EVQLYSGAERVKPKPGESELRLSCKGS	
b	1 EVQLYSGAERVKPKPGESELRLSCKGS	
b	61 SPSPFQQTISADKSISIATAYLQWSS	
y	61 SPSPFQQTISADKSISIATAYLQWSS	
y	61 SPSPFQQTISADKSISIATAYLQWSS	
b		

RESULT 7
 IS-09-490-324-40
 Sequence 40, Application US/09490324
 Patent No. 6828422
 GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pack, Peter
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Blueckthun, Andreas
 TITLE OF INVENTION: Protein (P)
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley
 STREET: 1251 Avenue of the
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatib.
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: PatentIn Release
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09
 FILING DATE: 24-Jan-2000
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09
 FILING DATE: 18-FEB-1998
 APPLICATION NUMBER: EP 95
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr.
 REGISTRATION NUMBER: 27,7
 REFERENCE DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 INFORMATION FOR SEQ ID NO: 40:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID N

RESULT 9
 US-09-025-769B-26
 Sequence 26, Application US/09025769B
 Patient No. 630064
 GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 APPLICANT: Pack, Peter
 APPLICANT: Ilag, Vic
 APPLICANT: Ge, Liming
 APPLICANT: Moroney, Simon
 APPLICANT: Plueckthun, Andreas
 TITLE OF INVENTION: Protein/ (Poly) peptide libraries
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,769B
 FILING DATE: 18-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Colin G. Sandercock, Esq.
 REGISTRATION NUMBER: 31,298
 REFERENCE/DOCKET NUMBER: 37629-0005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 912-2000
 TELEFAX: (202) 912-2020
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 US-09-490-070A-26

Query Match 89.1%; Score 553.5; DB 2; Length 119;
 Best Local Similarity 89.9%; Pred. No. 1.9e-48;
 Matches 107; Conservative 2; Nsmatches 7; Indels 3; Gaps 1;

RESULT 11
 US-09-490-153-26
 Sequence 26, Application US/09490070A
 Patient No. 6656248
 GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pack, Peter
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Plueckthun, Andreas

RESULT 10
 US-09-490-070A-26
 Sequence 26, Application US/09490070A
 Patient No. 6656248
 GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pack, Peter
 Ilag, Vic
 Ge, Liming

TITLE OF INVENTION: Protein/ (Poly) peptide libraries
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021

COMPUTER READABLE FORM:
 COMPUTER TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/490,153
 FILING DATE: 24-Jan-2000
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,769B
 FILING DATE: 16-FEB-1998
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 16-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)596-9000
 TELEFAX: (212)596-9090
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 US-09-490-153-26

Query Match 89.1%; Score 553.5; DB 2; Length 119;
 Best Local Similarity 89.9%; Pred. No. 1.9e-48;
 Matches 107; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

Qy 1 EVQLVSGAELVKPKPESLRSKCKGSDSPTTYWGVROMPGKCLEMMGLIYPGDSDTIY 60
 Db 1 EVQLVSGAELVKPKPESLRSKCKGSDSPTTYWGVROMPGKCLEMMGLIYPGDSDTIY 60

Qy 61 SPSRFQVTISADKSISTAYLQNSLKAASDAMYCTR --GDRGVDYWGQGTIVTVSS 116
 Db 61 SPSRFQVTISADKSISTAYLQNSLKAASDAMYCARLGGGYYFDWGGTIVTVSS 119

RESULT 13

US-09-920-262A-7

Sequence 7, Application US/09920262A
 Patent No. 6902734
 GENERAL INFORMATION:
 APPLICANT: Shealy, David
 APPLICANT: Knight, David
 APPLICANT: Scalton, Bernie
 APPLICANT: Giles-Komar, Jill
 APPLICANT: Perleit, David
 TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
 FILE REFERENCE: CEN0248
 CURRENT APPLICATION NUMBER: US/09/920,262A
 CURRENT FILING DATE: 2002-05-06
 PRIOR APPLICATION NUMBER: 60/1223,358
 PRIOR FILING DATE: 2000-08-07
 PRIOR APPLICATION NUMBER: 60/1236,827
 PRIOR FILING DATE: 2000-09-29
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: PatentIn Ver 3.1
 SEQ ID NO: 7
 LENGTH: 119
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-920-262A-7

Query Match 81.4%; Score 505.5; DB 2; Length 119;
 Best Local Similarity 80.7%; Pred. No. 1.3e-43;
 Matches 96; Conservative 9; Mismatches 11; Indels 3; Gaps 1;

Qy 1 EVQLVSGAELVKPKPESLRSKCKGSDSPTTYWGVROMPGKCLEMMGLIYPGDSDTIY 60
 Db 1 EVQLVSGAELVKPKPESLRSKCKGSDSPTTYWGVROMPGKCLEMMGLIYPGDSDTIY 60

Qy 61 SPSRFQVTISADKSISTAYLQNSLKAASDAMYCTR --GDRGVDYWGQGTIVTVSS 116
 Db 61 SPSRFQVTISADKSISTAYLQNSLKAASDAMYCARRPGQQYFDWGGTIVTVSS 119

RESULT 14

US 08-665-202-32
Sequence 32, Application US/08665202
Patent No. 5973322
GENERAL INFORMATION
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5973322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: United States

NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hause P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
Application number: 08/315, E74

COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patient in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60 /000,238
FILING DATE: 14-JUN-1996

FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

FORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

108 OCTLYVSS 116
121 OCTLYVSS 129

RESULT 15
US-09-315-574-32
Sequence 32, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TYPE OF INVENTION: Mammal Antigen

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OM protein - protein search, using SW model

Run on: December 3, 2005, 14:10:00 ; Search time 8.55102 Seconds
(without alignments)

Title: US-10-769-144-13

Perfect score: 33

Sequence: 1 TYWIG 5

Scoring table: BL0SUM62 Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21:
 1: GeneseqP1980s:
 2: GeneseqP1990s:
 3: GeneseqP2000s:
 4: GeneseqP2001s:
 5: GeneseqP2002s:
 6: GeneseqP2003as:
 7: GeneseqP2003bs:
 8: GeneseqP2004s:
 9: GeneseqP2005s:
 ...

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

25	33	100.0	248	5	ABP43990 Human BLY
26	33	100.0	248	7	Adg94817 Single ch
27	33	100.0	253	9	Adx01988 SARS coro
					Adx02018 SARS coro
28	33	100.0	254	9	ADX02018
29	33	100.0	254	9	ADX01958
30	33	100.0	254	9	ADX02020
31	33	100.0	254	9	ADX01960
32	33	100.0	254	9	ADX01962
33	33	100.0	254	9	ADX02028
					SARS coro
34	33	100.0	254	9	ADX01984
35	33	100.0	255	9	SARS coro
36	33	100.0	255	9	ADX01982
37	33	100.0	373	6	ABU5487
38	33	100.0	411	8	Abu5487
39	33	100.0	430	6	ADA34166
40	33	100.0	468	8	Adr46819
41	33	100.0	551	8	ADR46819
42	33	100.0	613	8	ADR46827
43	33	100.0	1627	8	ADN21185
44	32	97.0	78	7	ADC24839
45	32	97.0	116	3	AAB51824

ALIGNMENTS

ALIGNMENTS

RESULT 1

ADR46830

ID ADR46830 Standard; peptide; 5 AA.

XX

AC ADR46830;

XX

DT 18-NOV-2004 (first entry)

XX

DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

XX

molecular conjugate; monoclonal antibody; human antigen presenting cell;

KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;

KW betacG; beta chorionic gonadotropin; antibody;

KW cell-mediated immune response; immunisation; cytostatic; antimicrobial;

KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;

KW CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;

KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;

KW antibody B11; heavy chain variable region; CDR1; complementarity determining region.

XX

Homo sapiens.

OS Homo sapiens.

XX

PN WO200404074432-A2.

XX

PD 02-SEP-2004.

XX

PP 30-JAN-2004; 2004WO-US002725.

XX

PR 31-JAN-2003; 2003US-0443979P.

XX

(MEDA-) MEDAREX INC.

PA

Keller T, Endres M, He L, Ramakrishna V;

XX

PI 004-635555/61.

XX

PT New molecular conjugate having a monoclonal antibody that binds to human

CC APCs linked to a beta human chorionic gonadotropin, useful for inducing a

CC cytotoxic T cell response in cancers and infectious diseases.

XX

PS Claim 9; SEQ ID NO 13; 82pp; English.

XX

CC The present invention describes a molecular conjugate comprising a

CC monoclonal antibody that binds to human antigen presenting cells (APCs)

CC linked to beta human chorionic gonadotropin (betaCNG), where the antibody

CC comprises a heavy and/or light chain variable region, derived from a human

CC VH5-51 or Vk-L15 germline sequence with the 98 or 95 amino acid sequences

CC

Result No.	Query Score	Match Length	DB ID	Description
1	33	100.0	5 8 ADR46830	Adr46830 Human ant
2	33	100.0	5 8 ADR69905	Adr69905 Human IL-
3	33	100.0	5 9 ADY26777	Ady26777 Human ant
4	33	100.0	5 9 AEA18875	Aea18875 Amino aci
5	33	100.0	88 AAR22576	Aar22576 Heavy cha
6	33	100.0	109 8 ADI05782	Adi05782 Human mon
7	33	100.0	116 8 AAM48005	Aam48005 Human mon
8	33	100.0	116 8 ADR46821	Adr46821 Human ant
9	33	100.0	121 9 ADX02171	Adx02171 SARS coro
10	33	100.0	121 9 ADX02051	Adx02051 SARS coro
11	33	100.0	121 9 ADX02099	Adx02099 SARS coro
12	33	100.0	121 9 ADX02055	Adx02055 SARS coro
13	33	100.0	121 9 ADX02059	Adx02059 SARS coro
14	33	100.0	121 9 ADX02111	Adx02111 SARS coro
15	33	100.0	121 9 ADX02107	Adx02107 SARS coro
16	33	100.0	121 9 ADX02103	Adx02103 SARS coro
17	33	100.0	121 9 ADX02175	Adx02175 SARS coro
18	33	100.0	121 9 ADX02191	Adx02191 SARS coro
19	33	100.0	122 4 AAU02585	Aau02585 Anti-adip
20	33	100.0	125 9 ADY26764	Ady26764 Anti-NCF
21	33	100.0	130 6 ABP96715	Abp96715 Human ant
22	33	100.0	130 8 ADR69902	Adr69902 Human IL-
23	33	100.0	130 9 AEA18872	Aea18872 Amino aci
24	33	100.0	145 4 ABB65181	Abb65181 Drosophil

CC of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
 CC comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are
 CC linked to betahCG; (2) a molecular conjugate comprising a human single
 CC chain antibody that binds to human APCs linked to betahCG, where the
 CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
 (ADR46829); (3) a composition comprising any of the molecular conjugates
 CC as described above, and a carrier, optionally in combination with an
 CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
 CC against betahCG, comprising contacting any of the molecular conjugates
 CC described above with APCs such that the antigen is processed and
 CC presented to T cells in a manner which induces or enhances a T cell-
 CC mediated response against the antigen; (5) immunising a subject
 CC comprising administering any of the molecular conjugates described above,
 CC optionally in combination with an adjuvant, a cytokine which stimulates
 CC proliferation of dendritic cells and/or an immunostimulatory agent; and
 CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,
 CC comprising forming a conjugate of the antigen and a monoclonal antibody
 CC which binds to APCs, and contacting the conjugate either *in vivo* or *ex
vivo* with APCs such that the antigen is internalised, processed and
 CC presented to T cells in a manner which induces or enhances a cytotoxic T
 CC cell response against the antigen. The molecular conjugate has
 CC cytotoxic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
 CC virucide and antimalarial activities, and can be used as a CDR agonist,
 CC and in vaccines. The methods and compositions of the present invention
 CC are useful for inducing a cytotoxic T cell response, and in particular
 CC for treating autoimmune disorders, cancers and infectious diseases by
 CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
 CC including melanoma, fibrosarcoma, leukemia, malaria and
 CC herpes. The present sequence represents the human antibody B11 heavy
 CC chain variable region complementary determining region 1 (CDR1) amino
 CC acid sequence, which is used in the exemplification of the present
 CC invention.

XX Sequence 5 AA;

Query Match	Score	DB	Length
Best Local Similarity	100.0%	8	5;
Matches	100.0%	Pred. No. 2e+06;	
Qy	1 TYWIG 5	0;	
Db	1 TYWIG 5	0;	

OS Homo sapiens.

PN WO2004076620-A2.

XX 03-MAR-2005.

PD XX

PP 10-SEP-2004.

XX 15-JUL-2004; 2004WO-US022876.

PF XX

PR 25-FEB-2004; 2004WO-IB000484.

XX 15-JUL-2003; 2003US-0487431P.

PA XX (AMGEN INC.

PI Wild KD, Treanor JJS, Huang H, Inoue H, Zhang TJ, Martin F,

XX

PA (GENMAB AS.

XX Van De Winkel JGJ, Van Dijk MA, Schuurman J, Gerritsen AF;
 PI Baadsgaard Ods, Petersen J;
 XX DR WPI: 2004-6533191/63.

XX New isolated human monoclonal antibody that specifically binds to human IL-15, useful for diagnosing, preventing or treating lupus, ulcerative colitis, allograft rejection and graft-versus-host disease.

XX Claim 1: SEQ ID NO 5; 116pp; English.

PS The invention relates to a novel isolated human monoclonal antibody which specifically binds to human interleukin-15 (IL-15) comprising at least one CDR sequence from a fully defined sequence of 5, 17, 8, 12, 7 or 8 amino acids (ADR69305-ADR69910, respectively), a sequence at least 90, 95, 98 or 99% homologous to the amino acid sequences, or their fragments, which retain the ability to specifically bind to human IL-15. A monoclonal antibody of the invention has antiarthritic, ophthalmological, neuroprotective, nootropic, gastrointestinal, hepatotropic, antiallergic, haemopoietic, dermatoxic, immunosuppressive, cytotoxic, immunological, respiratory, gynaecological, and antimicrobial activity. The methods and compositions of the present invention are useful for the prevention and/or treatment of conditions associated with aberrant expression or activity of the IL-15, such as arthritis, connective tissue disorders, ophthalmological disorders, neurological disorders, gastrointestinal and cardiovascular, allergic disorders, haematologic disorders, malignant disorders, allergic disorders, skin disorders, pulmonary disorders, malignancies, transplantation-derived disorders, endocrinological disorders, vascular disorders, gynaecological disorders and infectious diseases, including ankylosing spondylitis, systemic lupus erythematosus, ulcerative colitis, allograft rejection and graft-versus-host disease. The present sequence represents CDR1 of the heavy chain variable (VH) region of a human IL-15 monoclonal antibody of the invention.

XX Sequence 5 AA;

CC The invention relates to a novel isolated human monoclonal antibody which
 CC specifically binds to human interleukin-15 (IL-15) comprising at least
 CC one CDR sequence from a fully defined sequence of 5, 17, 8, 12, 7 or 8
 CC amino acids (ADR69305-ADR69910, respectively), a sequence at least 90,
 CC 95, 98 or 99% homologous to the amino acid sequences, or their fragments,
 CC which retain the ability to specifically bind to human IL-15. A
 CC monoclonal antibody of the invention has antiarthritic, ophthalmological,
 CC neuroprotective, nootropic, gastrointestinal, hepatotropic, antiallergic,
 CC haemopoietic, dermatoxic, immunosuppressive, cytotoxic, immunological,
 CC respiratory, gynaecological, and antimicrobial activity. The methods and
 CC compositions of the present invention are useful for the prevention
 CC and/or treatment of conditions associated with aberrant expression or
 CC activity of the IL-15, such as arthritis, connective tissue disorders,
 CC ophthalmological disorders, neurological disorders, gastrointestinal and
 CC cardiovascular, allergic disorders, haematologic disorders, malignant
 CC disorders, skin disorders, pulmonary disorders, malignancies,
 CC transplantation-derived disorders, endocrinological disorders, vascular
 CC disorders, gynaecological disorders and infectious diseases, including
 CC ankylosing spondylitis, systemic lupus erythematosus, ulcerative colitis,
 CC allograft rejection and graft-versus-host disease. The present sequence
 CC represents CDR1 of the heavy chain variable (VH) region of a human IL-15
 CC monoclonal antibody of the invention.

XX Sequence 5 AA;

CC The invention relates to a novel isolated human monoclonal antibody which
 CC specifically binds to human interleukin-15 (IL-15) comprising at least
 CC one CDR sequence from a fully defined sequence of 5, 17, 8, 12, 7 or 8
 CC amino acids (ADR69305-ADR69910, respectively), a sequence at least 90,
 CC 95, 98 or 99% homologous to the amino acid sequences, or their fragments,
 CC which retain the ability to specifically bind to human IL-15. A
 CC monoclonal antibody of the invention has antiarthritic, ophthalmological,
 CC neuroprotective, nootropic, gastrointestinal, hepatotropic, antiallergic,
 CC haemopoietic, dermatoxic, immunosuppressive, cytotoxic, immunological,
 CC respiratory, gynaecological, and antimicrobial activity. The methods and
 CC compositions of the present invention are useful for the prevention
 CC and/or treatment of conditions associated with aberrant expression or
 CC activity of the IL-15, such as arthritis, connective tissue disorders,
 CC ophthalmological disorders, neurological disorders, gastrointestinal and
 CC cardiovascular, allergic disorders, haematologic disorders, malignant
 CC disorders, skin disorders, pulmonary disorders, malignancies,
 CC transplantation-derived disorders, endocrinological disorders, vascular
 CC disorders, gynaecological disorders and infectious diseases, including
 CC ankylosing spondylitis, systemic lupus erythematosus, ulcerative colitis,
 CC allograft rejection and graft-versus-host disease. The present sequence
 CC represents CDR1 of the heavy chain variable (VH) region of a human IL-15
 CC monoclonal antibody of the invention.

XX Sequence 5 AA;

CC The invention relates to a novel isolated human monoclonal antibody which
 CC specifically binds to human interleukin-15 (IL-15) comprising at least
 CC one CDR sequence from a fully defined sequence of 5, 17, 8, 12, 7 or 8
 CC amino acids (ADR69305-ADR69910, respectively), a sequence at least 90,
 CC 95, 98 or 99% homologous to the amino acid sequences, or their fragments,
 CC which retain the ability to specifically bind to human IL-15. A
 CC monoclonal antibody of the invention has antiarthritic, ophthalmological,
 CC neuroprotective, nootropic, gastrointestinal, hepatotropic, antiallergic,
 CC haemopoietic, dermatoxic, immunosuppressive, cytotoxic, immunological,
 CC respiratory, gynaecological, and antimicrobial activity. The methods and
 CC compositions of the present invention are useful for the prevention
 CC and/or treatment of conditions associated with aberrant expression or
 CC activity of the IL-15, such as arthritis, connective tissue disorders,
 CC ophthalmological disorders, neurological disorders, gastrointestinal and
 CC cardiovascular, allergic disorders, haematologic disorders, malignant
 CC disorders, skin disorders, pulmonary disorders, malignancies,
 CC transplantation-derived disorders, endocrinological disorders, vascular
 CC disorders, gynaecological disorders and infectious diseases, including
 CC ankylosing spondylitis, systemic lupus erythematosus, ulcerative colitis,
 CC allograft rejection and graft-versus-host disease. The present sequence
 CC represents CDR1 of the heavy chain variable (VH) region of a human IL-15
 CC monoclonal antibody of the invention.

XX Sequence 5 AA;

CC The invention relates to a novel isolated human monoclonal antibody which
 CC specifically binds to human interleukin-15 (IL-15) comprising at least
 CC one CDR sequence from a fully defined sequence of 5, 17, 8, 12, 7 or 8
 CC amino acids (ADR69305-ADR69910, respectively), a sequence at least 90,
 CC 95, 98 or 99% homologous to the amino acid sequences, or their fragments,
 CC which retain the ability to specifically bind to human IL-15. A
 CC monoclonal antibody of the invention has antiarthritic, ophthalmological,
 CC neuroprotective, nootropic, gastrointestinal, hepatotropic, antiallergic,
 CC haemopoietic, dermatoxic, immunosuppressive, cytotoxic, immunological,
 CC respiratory, gynaecological, and antimicrobial activity. The methods and
 CC compositions of the present invention are useful for the prevention
 CC and/or treatment of conditions associated with aberrant expression or
 CC activity of the IL-15, such as arthritis, connective tissue disorders,
 CC ophthalmological disorders, neurological disorders, gastrointestinal and
 CC cardiovascular, allergic disorders, haematologic disorders, malignant
 CC disorders, skin disorders, pulmonary disorders, malignancies,
 CC transplantation-derived disorders, endocrinological disorders, vascular
 CC disorders, gynaecological disorders and infectious diseases, including
 CC ankylosing spondylitis, systemic lupus erythematosus, ulcerative colitis,
 CC allograft rejection and graft-versus-host disease. The present sequence
 CC represents CDR1 of the heavy chain variable (VH) region of a human IL-15
 CC monoclonal antibody of the invention.

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CC The invention relates to a novel isolated human monoclonal antibody which
 CC specifically binds to human interleukin-15 (IL-15) comprising at least
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 CC amino acids (ADR69305-ADR69910, respectively), a sequence at least 90,
 CC 95, 98 or 99% homologous to the amino acid sequences, or their fragments,
 CC which retain the ability to specifically bind to human IL-15. A
 CC monoclonal antibody of the invention has antiarthritic, ophthalmological,
 CC neuroprotective, nootropic, gastrointestinal, hepatotropic, antiallergic,
 CC haemopoietic, dermatoxic, immunosuppressive, cytotoxic, immunological,
 CC respiratory, gynaecological, and antimicrobial activity. The methods and
 CC compositions of the present invention are useful for the prevention
 CC and/or treatment of conditions associated with aberrant expression or
 CC activity of the IL-15, such as arthritis, connective tissue disorders,
 CC ophthalmological disorders, neurological disorders, gastrointestinal and
 CC cardiovascular, allergic disorders, haematologic disorders, malignant
 CC disorders, skin disorders, pulmonary disorders, malignancies,
 CC transplantation-derived disorders, endocrinological disorders, vascular
 CC disorders, gynaecological disorders and infectious diseases, including
 CC ankylosing spondylitis, systemic lupus erythematosus, ulcerative colitis,
 CC allograft rejection and graft-versus-host disease. The present sequence
 CC represents CDR1 of the heavy chain variable (VH) region of a human IL-15
 CC monoclonal antibody of the invention.

XX Sequence 5 AA;

CC The invention relates to a novel isolated human monoclonal antibody which
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 CC amino acids (ADR69305-ADR69910, respectively), a sequence at least 90,
 CC 95, 98 or 99% homologous to the amino acid sequences, or their fragments,
 CC which retain the ability to specifically bind to human IL-15. A
 CC monoclonal antibody of the invention has antiarthritic, ophthalmological,
 CC neuroprotective, nootropic, gastrointestinal, hepatotropic, antiallergic,
 CC haemopoietic, dermatoxic, immunosuppressive, cytotoxic, immunological,
 CC respiratory, gynaecological, and antimicrobial activity. The methods and
 CC compositions of the present invention are useful for the prevention
 CC and/or treatment of conditions associated with aberrant expression or
 CC activity of the IL-15, such as arthritis, connective tissue disorders,
 CC ophthalmological disorders, neurological disorders, gastrointestinal and
 CC cardiovascular, allergic disorders, haematologic disorders, malignant
 CC disorders, skin disorders, pulmonary disorders, malignancies,
 CC transplantation-derived disorders, endocrinological disorders, vascular
 CC disorders, gynaecological disorders and infectious diseases, including
 CC ankylosing spondylitis, systemic lupus erythematosus, ulcerative colitis,
 CC allograft rejection and graft-versus-host disease. The present sequence
 CC represents CDR1 of the heavy chain variable (VH) region of a human IL-15
 CC monoclonal antibody of the invention.

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 CC one CDR sequence from a fully defined sequence of 5, 17, 8, 12, 7 or 8
 CC amino acids (ADR69305-ADR69910, respectively), a sequence at least 90,
 CC 95, 98 or 99% homologous to the amino acid sequences, or their fragments,
 CC which retain the ability to specifically bind to human IL-15. A
 CC monoclonal antibody of the invention has antiarthritic, ophthalmological,
 CC neuroprotective, nootropic, gastrointestinal, hepatotropic, antiallergic,
 CC haemopoietic, dermatoxic, immunosuppressive, cytotoxic, immunological,
 CC respiratory, gynaecological, and antimicrobial activity. The methods and
 CC compositions of the present invention are useful for the prevention
 CC and/or treatment of conditions associated with aberrant expression or
 CC activity of the IL-15, such as arthritis, connective tissue disorders,
 CC ophthalmological disorders, neurological disorders, gastrointestinal and
 CC cardiovascular, allergic disorders, haematologic disorders, malignant
 CC disorders, skin disorders, pulmonary disorders, malignancies,
 CC transplantation-derived disorders, endocrinological disorders, vascular
 CC disorders, gynaecological disorders and infectious diseases, including
 CC ankylosing spondylitis, systemic lupus erythematosus, ulcerative colitis,
 CC allograft rejection and graft-versus-host disease. The present sequence
 CC represents CDR1 of the heavy chain variable (VH) region of a human IL-15
 CC monoclonal antibody of the invention.

XX Sequence 5 AA;

CC The invention relates to a novel isolated human monoclonal antibody which
 CC specifically binds to human interleukin-15 (IL-15) comprising at least
 CC one CDR sequence from a fully defined sequence of 5, 17, 8, 12, 7 or 8
 CC amino acids (ADR69305-ADR69910, respectively), a sequence at least 90,
 CC 95, 98 or 99% homologous to the amino acid sequences, or their fragments,
 CC which retain the ability to specifically bind to human IL-15. A
 CC monoclonal antibody of the invention has antiarthritic, ophthalmological,
 CC neuroprotective, nootropic, gastrointestinal, hepatotropic, antiallergic,
 CC haemopoietic, dermatoxic, immunosuppressive, cytotoxic, immunological,
 CC respiratory, gynaecological, and antimicrobial activity. The methods and
 CC compositions of the present invention are useful for the prevention
 CC and/or treatment of conditions associated with aberrant expression or
 CC activity of the IL-15, such as arthritis, connective tissue disorders,
 CC ophthalmological disorders, neurological disorders, gastrointestinal and
 CC cardiovascular, allergic disorders, haematologic disorders, malignant
 CC disorders, skin disorders, pulmonary disorders, malignancies,
 CC transplantation-derived disorders, endocrinological disorders, vascular
 CC disorders, gynaecological disorders and infectious diseases, including
 CC ankylosing spondylitis, systemic lupus erythematosus, ulcerative colitis,
 CC allograft rejection and graft-versus-host disease. The present sequence
 CC represents CDR1 of the heavy chain variable (VH) region of a human IL-15
 CC monoclonal antibody of the invention.

XX Sequence 5 AA;

RESULT 3
 ADY26777

ID ADY26777 standard; protein; 5 AA.

XX AC ADY26777;

XX DT 19-MAY-2005 (first entry)

XX DB Human anti-NGF-antibody heavy chain CDR1 SEQ ID NO 92.

XX KW analgesic; gene therapy; antibody engineering; pharmaceutical; pain;

XX neurological disease; NGF; nerve growth factor; heavy chain; CDR1.

XX OS Homo sapiens.

XX PN WO2005019266-A2.

XX PD 03-MAR-2005.

XX PP 15-JUL-2004; 2004WO-US022876.

XX PR 15-JUL-2003; 2003US-0487431P.

XX PA (AMGEN INC.

XX PI Wild KD, Treanor JJS, Huang H, Inoue H, Zhang TJ, Martin F,

XX PA (GENMAB AS.

DR WPI; 2005-202606/21.
 PT New human anti-nerve growth factor (NGF) neutralizing antibodies useful
 PT for manufacturing a medicament for treating painful disorders (e.g. acute
 PT pain) or conditions associated with increased expression or sensitivity
 PT to NGF.
 XX SEQ ID NO 92; 190pp; English.

CC The invention describes an isolated human antibody that interacts with or binds specifically to human nerve growth factor (NGF) and neutralize the function of NGF. Also described are: methods of treating a condition caused by increased expression of NGF or increased sensitivity to NGF in a patient; methods for detecting NGF in a biological sample; an NGF specific binding agent comprising any of the 59 amino acid sequences comprising, for e.g., 123, 107 or 14 amino acids, as mentioned in the specification, and where the binding agent can bind to NGF; a pharmaceutical composition comprising a pharmaceutical carrier and a therapeutic amount of the antibody or binding agent cited above; or a medicament for treating a painful disorder or condition associated with increased expression of NGF or increased sensitivity to NGF, the medicament comprising a pharmaceutical amount of a monoclonal antibody or its immunologically functional immunoglobulin fragment, or pharmaceutical salts of the monoclonal antibody or the fragment, where the monoclonal antibody is at least one of the monoclonal antibody cited above, and a pharmaceutical carrier, diluent or excipient; a nucleic acid molecule or polynucleotide that encodes the above antibody or binding agent; an isolated cell line that produces the above antibody or binding agent; an expression vector comprising the above polynucleotide; and a host cell comprising the nucleic acid or expression vector. The composition (including the antibody) and methods are useful for manufacturing a medicament for treating a painful disorder (e.g. acute pain, dental pain, or pain from trauma or cancer), or a condition associated with increased expression of NGF or increased sensitivity to NGF. This is the amino acid sequence of a human NGF antibody heavy chain complementarity determining region 1 (CDR1).
 XX Sequence 5 AA;

Query Match 100.0%; Score 33; DB 9; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
 Db 1 TYWIG 5

RESULT 4
 AEA18875 standard; Peptide: 5 AA.
 ID AEA18875
 AC AEA18875;
 DT 28-JUL-2005 (first entry)
 XX Amino acid sequence of anti-IL-15 antibody CDR peptide #1.
 KW monocyte; interleukin-15; IL-15; IL-15 antagonist; apoptosis; gout;
 KW connective tissue disorder; neuroprotective; antigen; inflammation;
 KW musculoskeletal disease; gastrointestinal-gen.; muscular-gen.; cardiotropic;
 KW antiallergic; immune disorder; respiratory-gen.; neoplasm; cytostatic;
 KW endocrine-gen.; vasoconstrictive; antiinflammatory; cardiovascular disease;
 KW antianemic; antimicrobial; infection; osteopathic; neurological disease;
 KW gastrointestinal disease; hepatic disease; allergy;
 KW hematological disease; dermatological disease; pulmonary disease;
 KW prostatic cancer; endocrine disease; vasculitis; infectious disease;
 KW renal disease; muscle disease; cardiac disorder; circulatory disorder;
 KW blood clotting disorder; bone disease;
 KW complementarity determining region; CDR.
 XX Homo sapiens.

OS Homo sapiens.
 XX

PN WO2005044303-A1.
 XX 19-MAY-2005.
 PD 05-NOV-2004; 2004WO-IB003895.
 PR 06-NOV-2003; 2003US-0518552P.
 PA (GENM-) GENMAB AS.
 XX Beurskens F, Schuurman J, Parren P, Petersen J, Baadsgaard ODM.
 PI DR WPI; 2005-356210/36.
 XX PT Treating diseases involving monocytic activity (e.g. cancer, neurological, hematological, cardiac or metabolic disorders) comprises administering an interleukin-15 antagonist that induces apoptosis of monocytes.
 XX PT Claim 27; SEQ ID NO 5; 38pp; English.
 CC The specification describes a method of treating a disease involving monocytic activity. The method comprises administering an interleukin-15 (IL-15) antagonist that induces apoptosis of monocyte. The antagonist is an agent that binds to IL-15 or IL-15R (interleukin-15 receptor), e.g. an antibody. The method is useful for treating disorders involving monocytic activity, such as gout, connective disorder, neurological diseases, gastrointestinal or hepatic diseases, allergies, hematological diseases, dermatological diseases, pulmonary diseases, prostatic cancer, endocrine diseases, vasculitis, infectious diseases, renal diseases, muscle diseases, cardiac disorders, circulatory disorders, blood clotting disorder, and bone diseases. AEA18875-AEA18880 represent complementarity determining regions (CDRs) derived from an anti-IL-15 antibody. This antibody may be used in the method of the invention.
 XX PS Sequence 5 AA;
 CC Query Match 100.0%; Score 33; DB 9; Length 5;
 CC Best Local Similarity 100.0%; Pred. No. 2e+06;
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC Qy 1 TYWIG 5
 CC Db 1 TYWIG 5

RESULT 5
 AAR22576
 ID AAR22576 standard; protein: 88 AA.
 XX AC AAR22576;
 XX DT 23-SEP-2004 (revised)
 XX DT 21-MAY-1992 (first entry)
 XX DB Heavy chain VH16.1 from lysozyme binding scFv fragment.
 XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
 KW g3p; binding; adsorption; gene VII; diverse repertoire;
 KW specific binding pairs; replicable genetic display package; human.
 XX Homo sapiens.
 OS Unidentified.
 XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
 KW g3p; binding; adsorption; gene VII; diverse repertoire;
 KW specific binding pairs; replicable genetic display package; human.
 XX WO9201047-A.
 XX PD 23-JAN-1992.
 XX PP 1-0-JUL-1990; 90GB-00015198.
 XX PR 10-JUL-1990; 90GB-00015198.
 PR 19-OCT-1990; 90GB-00023845.
 PR 12-NOV-1990; 90GB-00024503.

PR 06-MAR-1991; 91GB-00004744.
 PR 15-MAY-1991; 91GB-00010549.
 XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PA (MEDI-) MED RES COUNCIL.
 XX
 PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
 PI Jackson RH, Holliger KP, Marks JD;
 XX DR WPI; 1992-056882/07.
 XX PT Producing members of specific binding pairs - by expression in recombinant host cells with a secreting replicable genetic display package.
 XX PS Disclosure; Page ?; 209pp; English.
 XX PCR was used to prepare a human scFv library from RNA from white blood cells from an unimmunised donor. Heavy chains from IgG and IgM antibodies were amplified separately. Four separate libraries were generated (IgG-K, IgG-Lambda, IgM-K and IgM-Lambda). The purified scFv fragments were ligated into the phagemid pHENI for expression on the surface of fd bacteriophage as gene III fusions. The clones were then subjected to affinity selection for binding to lysosome binding clones were identified. >95% being from the IgM library. The clones gave three different BstNI restriction patterns, and at least 2 clones from each pattern was sequenced. The sequences indicated the presence of 4 unique human VH-VL combinations. The sequence shown here is one of the VH chains found. See also AAR21260-307, 309-312, AAR22450, AAR22565, AAR22567-81
 CC Revised record issued on 23-SEP-2004 : Correction to sequence location
 XX SQ Sequence 88 AA;
 Query Match 100.0%; Score 33; DB 2; Length 88;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TYWIG 5
 Db 31 TYWIG 35
 XX RESULT 6
 ADI05782 Human monoclonal antibody CM-2 variable region heavy chain, SEQ ID 12.
 ID ADI05782 standard; protein; 109 AA.
 XX Cytostatic; Gene therapy; neoplasm; antibody; variable region;
 KW heavy chain; proliferative disorder; human; CM-2.
 XX OS Homo sapiens.
 XX FH Location/Qualifiers
 FT Region 16. .22
 FT /label= CDR1
 FT Region 40. .47
 FT /label= CDR2
 FT Region 86. .100
 FT /label= CDR3
 XX PN WO2004005351-A2.
 XX PD 15-JAN-2004.
 XX PP 02-JUL-2003; 2003WO-IB003487.
 PR 04-JUL-2002; 2002DE-01049906.
 PR 04-JUL-2002; 2002DE-01029907.
 PR 06-JUL-2002; 2002DE-01030516.
 XX (ONCO-) ONCOMAB GMBH.
 XX PI Mueller-Hermelink H, Vollmers H;
 XX DR WPI; 2004-12275/12.
 DR N-PSDB; ADI05781.
 XX PT New purified polypeptides (e.g. an antibody) that induces apoptosis of a neoplastic cell, useful for diagnosing or treating a neoplasm or a proliferative disorder in mammals, including humans.
 XX PS Claim 93; SEQ ID NO 12; 106pp; English.
 XX CC The present invention relates to neoplasm specific antibody variable region light and heavy chain sequences (ADI05771-AD105782). The antibody sequences are useful in diagnosing or treating a neoplasm or a proliferative disorder in a mammal.
 CC SQ Sequence 109 AA;
 Query Match 100.0%; Score 33; DB 8; Length 109;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TYWIG 5
 Db 20 TYWIG 24
 XX RESULT 7
 AAM48005 Human monoclonal antibody B11 variable heavy chain protein.
 ID AAM48005 standard; protein; 116 AA.
 XX AC AAM48005;
 XX DT 08-MAR-2002 (first entry)
 XX DE Human monoclonal antibody B11 variable heavy chain protein.
 XX KW Human; monoclonal antibody; B11; antigen binding portion; dendritic cell; KW mannose receptor; growth; cytolytic; KW pathogen; virus; bacterium;
 KW autoimmune disease; inflammatory disorder; rheumatoid arthritis;
 KW multiple sclerosis; diabetes mellitus; immunomodulatory;
 KW antiinflammatory; antirheumatic; immunoprotective;
 KW antidiabetic; antianemic; endocrine; dermatological; antithyroid;
 KW uropathic; ophthalmological; muscular.
 XX OS Homo sapiens.
 XX PN WO200185798-A2.
 XX PD 15-NOV-2001.
 XX PP 08-MAY-2001; 2001WO-US05114.
 XX PR 08-MAY-2000; 2000US-020126P.
 PR 07-SEP-2000; 2000US-0230739P.
 XX (MEDA-) MEDAREX INC.
 PA Deo YM, Keler T;
 XX PI
 DR WPI; 2002-089788/12.
 DR N-PSDB; ABA05500.
 XX PT New human monoclonal antibodies specific for dendritic cells, useful for PT inhibiting growth or inducing cytolysis of a dendritic cell and treating PT or preventing a dendritic cell mediated disease, e.g., autoimmune disorders.

Example 2; Fig 13; 95pp; English.

The invention relates to human monoclonal antibodies or their antigen binding portions that specifically bind to dendritic cells and has one or more of the following characteristics: (a) a binding affinity constant to a dendritic cell of at least about 10⁷ M⁻¹; (b) the ability to opsonise a dendritic cell; (c) the ability to internalise after binding to dendritic cells; or (d) the ability to activate dendritic cells. The isolated human monoclonal antibody or its antigen binding portion may also have any of the following characteristics: (a) mediates cytolysis of dendritic cells in the presence of human effector cells; or (b) inhibits growth of dendritic cells. The antibodies or their antigen binding portion, binds to and blocks the human mannose receptor on dendritic cells. The antibodies have immunomodulatory, antiinflammatory, antirheumatic, antiarthritic, neuroprotective, antidiabetic, antianæmic, endocrine, dermatological, antithyroid, uropathic, ophthalmological and muscular activity. The antibodies or their antigen-binding fragments are useful for inhibiting growth of a dendritic cell, inducing cytolysis of a dendritic cell, treating or preventing a dendritic cell mediated disease, detecting the presence of a dendritic cell, targeting an antigen to a dendritic cell and preventing binding of a pathogen (a virus or a bacterium) to human mannose receptor on dendritic cells. In particular, the antibodies may be used to treat, autoimmune disease, graft versus host disease, immune system or inflammatory disorders (e.g. rheumatoid arthritis), multiple sclerosis, diabetes mellitus, myasthenia gravis, pernicious anaemia, Addison's disease, lupus erythematosus, Reiter's syndrome and Graves' disease. The present sequence is that of the human monoclonal antibody B11 variable heavy chain, useful to the invention Sequence 116 AA;

Query Match 100.0%; Score 33; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 31 TWIG 35

RESULT 8
ADR46821
ID ADR46821 Standard; protein; 116 AA.
XX DT 18-NOV-2004 (First entry)

DB Human antibody B11 heavy chain variable region protein SEQ ID NO:4.
XX molecular conjugate; monoclonal antibody; human antigen presenting cell; KW antigen presenting cell; AC; human; beta human chorionic gonadotropin; betahCG; beta chorionic gonadotropin; antibody; T cell mediated immune response; immunisation; cytostatic; antimicrobial; KW immuno suppressive; anti-HIV; hepatotoxic; virucide; antimarial; CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease; KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes; KW antibody B11; heavy chain variable region.
XX Homo sapiens.
OS WO2004074432-A2.

XX 02-SEP-2004.

XX 30-JAN-2004; 2004WO-US002725.

XX 31-JAN-2003; 2003US-0443979P.

XX (MEDA-) MEDAREX INC.

XX Keler T, Endres M, He L, Ramakrishna V;

XX WPI; 2004-635555/61.
PS DR N-PSDB; ADR46820.

XX New molecular conjugate having a monoclonal antibody that binds to human APCs linked to a beta human chorionic gonadotropin, useful for inducing a cytotoxic T cell response in cancers and infectious diseases.

XX Claim 11; SEQ ID NO 4; 82pp; English.

XX The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (APCs) linked to beta human chorionic gonadotropin (betaHCG), where the antibody comprises a heavy and/or light chain variable region derived from a human VH5-51 or Vk-L15 germline sequence with the 98 or 95 amino acid sequences of SEQ ID NO:30 or 32 (ADR4684¹, or ADR4684²), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are linked to betaHCG; (2) a molecular conjugate comprising a human single chain antibody that binds to human APCs linked to betaHCG, where the conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an adjuvant; (4) inducing or enhancing a T cell-mediated immune response, against betaHCG, comprising contacting any of the molecular conjugates described above with APCs such that the antigen is processed and presented to T cells in a manner which induces or enhances a T cell-mediated response against the antigen; (5) immunising a subject comprising administering any of the molecular conjugates described above, optionally in combination with an adjuvant, a cytokine which stimulates proliferation of dendritic cells and/or an immunomodulatory agent; and (6) inducing or enhancing cytotoxic T cell response against an antigen, comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either in vivo or ex vivo with APCs such that the antigen is internalised, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate has cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotoxic, virucide and antimalarial activities, and can be used as a CD8 agonist, and in vaccines. The methods and compositions of the present invention are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The Present sequence represents a human antibody B11 heavy chain variable region, which is used in the exemplification of the present invention.

XX SQ Sequence 116 AA;

Query Match 100.0%; Score 33; DB 8; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.1e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 31 TWIG 35

RESULT 9
ADX02171 Standard; protein; 121 AA.

XX ADX02171;

XX AC ADX02171;

XX DT 21-APR-2005 (first entry)

XX SARS coronavirus antibody heavy chain SEQ ID NO 427.
KW severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide; KW respiratory disease; infection; antibody; heavy chain.
XX OS SARS coronavirus.

XX WO2005012360-A2.
 XX PR 01-SEP-2003; 2003WO-EP050391.
 XX PR 16-OCT-2003; 2003WO-EP050723.
 XX PR 24-NOV-2003; 2003WO-EP050883.
 XX PR 04-DEC-2003; 2003WO-EP050943.
 XX PR 02-FEB-2004; 2004WO-EP05067.
 XX PR 13-FEB-2004; 2004WO-EP05127.
 XX PR 19-MAR-2004; 2004WO-EP05334.
 XX PR 07-APR-2004; 2004WO-EP050464.
 XX PR 14-APR-2004; 2004WO-EP050516.
 XX PR 29-APR-2004; 2004WO-EP050643.
 XX PA (CRUC-) CRUCELL HOLLAND BV.
 XX PI Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudsmit J;
 XX DR WPI; 2005-142879/15.
 XX DR N-PDB; ADX02050.
 XX PT New binding molecules that specifically bind to severe acute respiratory syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or treating conditions resulting from SARS-CoV.
 XX PS Claim 4; SEQ ID NO 307; 633pp; English.
 XX PS PT
 XX CC The invention relates to a binding molecule, or its variant, capable of specifically binding to a severe acute respiratory syndrome (SARS)-coronavirus (CoV). The composition (including the binding molecule or its functional variant, or the immunoconjugate) is useful as a medicament for the diagnosis, prophylaxis or treatment of a condition resulting from a SARS-CoV, or in the preparation of the medicament. The present sequence represents a SARS coronavirus binding molecule heavy chain.
 XX SQ Sequence 121 AA;
 XX Query Match Similarity 100.0%; Score 33; DB 9; Length 121;
 XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX ID ADX02099 standard; protein; 121 AA.
 XX ID ADX02099;
 XX AC ADX02099;
 XX DT 21-APR-2005 (first entry)
 XX XX SARS coronavirus antibody heavy chain SEQ ID NO 355.
 XX DE WO2005012360-A2.
 XX KW severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide; respiratory disease; infection; antibody; heavy chain.
 XX AC ADX02051;
 XX DT 21-APR-2005 (first entry)
 XX DE SARS coronavirus antibody heavy chain SEQ ID NO 307.
 XX KW severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide; respiratory disease; infection; antibody; heavy chain.
 XX OS SARS coronavirus.
 XX PR 22-JUL-2003; 2003WO-EP050328.
 XX PR 01-SEP-2003; 2003WO-EP050391.
 XX PR 16-OCT-2003; 2003WO-EP050723.
 XX PR 24-NOV-2003; 2003WO-EP050883.
 XX PR 04-FEB-2004; 2004WO-EP050943.
 XX PR 02-FEB-2004; 2004WO-EP05067.
 XX PR 13-FEB-2004; 2004WO-EP05127.
 XX PR 19-MAR-2004; 2004WO-EP05334.
 XX PR 07-APR-2004; 2004WO-EP050464.
 XX PR 14-APR-2004; 2004WO-EP050516.
 XX PR 29-APR-2004; 2004WO-EP050643.
 XX PA (CRUC-) CRUCELL HOLLAND BV.
 XX PI Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudsmit J;
 XX DR WPI; 2005-142879/15.
 XX DR N-PDB; ADX02050.
 XX PT New binding molecules that specifically bind to severe acute respiratory syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or treating conditions resulting from SARS-CoV.
 XX PS Claim 4; SEQ ID NO 307; 633pp; English.
 XX PS PT
 XX CC The invention relates to a binding molecule, or its variant, capable of specifically binding to a severe acute respiratory syndrome (SARS)-coronavirus (CoV). The composition (including the binding molecule or its functional variant, or the immunoconjugate) is useful as a medicament for the diagnosis, prophylaxis or treatment of a condition resulting from a SARS-CoV, or in the preparation of the medicament. The present sequence represents a SARS coronavirus binding molecule heavy chain.
 XX SQ Sequence 121 AA;
 XX Query Match Similarity 100.0%; Score 33; DB 9; Length 121;
 XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX ID ADX02099 standard; protein; 121 AA.
 XX ID ADX02099;
 XX AC ADX02099;
 XX DT 21-APR-2005 (first entry)
 XX XX SARS coronavirus antibody heavy chain SEQ ID NO 355.
 XX DE WO2005012360-A2.
 XX KW severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide; respiratory disease; infection; antibody; heavy chain.
 XX AC ADX02051;
 XX DT 21-APR-2005 (first entry)
 XX DE SARS coronavirus antibody heavy chain SEQ ID NO 307.
 XX KW severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide; respiratory disease; infection; antibody; heavy chain.
 XX OS SARS coronavirus.
 XX PR 22-JUL-2003; 2003WO-EP050328.
 XX PR 01-SEP-2003; 2003WO-EP050391.
 XX PR 16-OCT-2003; 2003WO-EP050723.
 XX PR 24-NOV-2003; 2003WO-EP050883.
 XX PR 04-FEB-2004; 2004WO-EP050943.
 XX PR 02-FEB-2004; 2004WO-EP05067.
 XX PR 13-FEB-2004; 2004WO-EP05127.
 XX PR 19-MAR-2004; 2004WO-EP05334.
 XX PR 07-APR-2004; 2004WO-EP050464.
 XX PR 14-APR-2004; 2004WO-EP050516.
 XX PR 29-APR-2004; 2004WO-EP050643.
 XX PA (CRUC-) CRUCELL HOLLAND BV.
 XX PI Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudsmit J;
 XX DR WPI; 2005-142879/15.
 XX DR N-PDB; ADX02050.
 XX PT New binding molecules that specifically bind to severe acute respiratory syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or treating conditions resulting from SARS-CoV.
 XX PS Claim 4; SEQ ID NO 307; 633pp; English.
 XX PS PT
 XX CC The invention relates to a binding molecule, or its variant, capable of specifically binding to a severe acute respiratory syndrome (SARS)-coronavirus (CoV). The composition (including the binding molecule or its functional variant, or the immunoconjugate) is useful as a medicament for the diagnosis, prophylaxis or treatment of a condition resulting from a SARS-CoV, or in the preparation of the medicament. The present sequence represents a SARS coronavirus binding molecule heavy chain.
 XX SQ Sequence 121 AA;
 XX Query Match Similarity 100.0%; Score 33; DB 9; Length 121;
 XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX ID ADX02099 standard; protein; 121 AA.
 XX ID ADX02099;
 XX AC ADX02099;
 XX DT 21-APR-2005 (first entry)
 XX XX SARS coronavirus antibody heavy chain SEQ ID NO 355.
 XX DE WO2005012360-A2.
 XX KW severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide; respiratory disease; infection; antibody; heavy chain.
 XX AC ADX02051;
 XX DT 21-APR-2005 (first entry)
 XX DE SARS coronavirus antibody heavy chain SEQ ID NO 307.
 XX KW severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide; respiratory disease; infection; antibody; heavy chain.
 XX OS SARS coronavirus.
 XX PR 22-JUL-2003; 2003WO-EP050328.
 XX PR 01-SEP-2003; 2003WO-EP050391.
 XX PR 16-OCT-2003; 2003WO-EP050723.
 XX PR 24-NOV-2003; 2003WO-EP050883.
 XX PR 04-FEB-2004; 2004WO-EP050943.
 XX PR 02-FEB-2004; 2004WO-EP05067.
 XX PR 13-FEB-2004; 2004WO-EP05127.
 XX PR 19-MAR-2004; 2004WO-EP05334.
 XX PR 07-APR-2004; 2004WO-EP050464.

CC The invention relates to a binding molecule, or its variant, capable of
 CC specifically binding to a severe acute respiratory syndrome (SARS)-
 CC coronavirus (CoV). The composition (including the binding molecule or its
 CC functional variant, or the immunoconjugate) is useful as a medicament for
 CC the diagnosis, prophylaxis or treatment of a condition resulting from a
 CC SARS-CoV, or in the preparation of the medicament. The present sequence
 CC represents a SARS coronavirus binding molecule heavy chain.
 XX Sequence 121 AA;

SQ Sequence 121 AA;
 Query Match 100.0%; Score 33; DB 9; Length 121;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX ADX02111 standard; protein; 121 AA.

Qy 1 TYWIG 5
 AC |||||
 Db 33 TYWIG 37

Query Match 100.0%; Score 33; DB 9; Length 121;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX ADX02111 standard; protein; 121 AA.

Qy 1 TYWIG 5
 AC |||||
 Db 33 TYWIG 37

RESULT 14

ADX02111
 ID ADX02111 standard; protein; 121 AA.

XX AC |||||
 XX DT 21-APR-2005 (first entry)

XX DB SARS coronavirus antibody heavy chain SEQ ID NO 363.

XX Qy 1 TYWIG 5
 AC |||||
 Db 33 TYWIG 37

Query Match 100.0%; Score 33; DB 9; Length 121;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX ADX02107
 ID ADX02107 standard; protein; 121 AA.

Qy 1 TYWIG 5
 AC |||||
 Db 33 TYWIG 37

RESULT 15

ADX02111
 ID ADX02111 standard; protein; 121 AA.

XX AC |||||
 XX DT 21-APR-2005 (first entry)

XX DB SARS coronavirus antibody heavy chain SEQ ID NO 363.

XX Qy 1 TYWIG 5
 AC |||||
 Db 33 TYWIG 37

Query Match 100.0%; Score 33; DB 9; Length 121;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX ADX02107
 ID ADX02107 standard; protein; 121 AA.

Qy 1 TYWIG 5
 AC |||||
 Db 33 TYWIG 37

RESULT 16

ADX02111
 ID ADX02111 standard; protein; 121 AA.

XX AC |||||
 XX DT 21-APR-2005 (first entry)

XX DB SARS coronavirus antibody heavy chain SEQ ID NO 363.

XX Qy 1 TYWIG 5
 AC |||||
 Db 33 TYWIG 37

Query Match 100.0%; Score 33; DB 9; Length 121;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX ADX02107
 ID ADX02107 standard; protein; 121 AA.

Qy 1 TYWIG 5
 AC |||||
 Db 33 TYWIG 37

RESULT 17

ADX02111
 ID ADX02111 standard; protein; 121 AA.

XX AC |||||
 XX DT 21-APR-2005 (first entry)

XX DB SARS coronavirus antibody heavy chain SEQ ID NO 363.

XX Qy 1 TYWIG 5
 AC |||||
 Db 33 TYWIG 37

Query Match 100.0%; Score 33; DB 9; Length 121;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX ADX02107
 ID ADX02107 standard; protein; 121 AA.

Qy 1 TYWIG 5
 AC |||||
 Db 33 TYWIG 37

Query Match 100.0%; Score 33; DB 9; Length 121;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX ADX02107
 ID ADX02107 standard; protein; 121 AA.

Qy 1 TYWIG 5
 AC |||||
 Db 33 TYWIG 37

Query Match 100.0%; Score 33; DB 9; Length 121;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX ADX02107
 ID ADX02107 standard; protein; 121 AA.

Qy 1 TYWIG 5
 AC |||||
 Db 33 TYWIG 37

Db 33 TYWIG 37

Search completed: December 3, 2005, 14:25:04
Job time : 9.55102 Secs

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RESULT 3
Qy 1 TYWIG 5
Db 35 TYWIG 39

A: Molecule type: mRNA
A: Residues: 1-119 <GRI>
A: Cross-references: UNIPARC:UPI00001180B9; EMBL:218848; NID:933122; PIDN:CAA79300.1; PID: F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0% Score 33; DB 2; Length 119;
Best Local Similarity 100.0%; **Pred.** No. 33;
Matches 5; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Qy 1 TYWIG 5
Db 31 TYWIG 35

A: Molecule type: mRNA
A: Residues: 1-102 <CAI>
A: Cross-references: UNIPARC:UPI0000176BD0

A: Experimental source: EBV-transformed CD5+ B cell [from adult PBL]
C: Superfamily: immunoglobulin V region; immunoglobulin homology
C: Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Query Match 100.0% Score 33; DB 2; Length 102;
Best Local Similarity 100.0%; **Pred.** No. 28;
Matches 5; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Qy 1 TYWIG 5
Db 35 TYWIG 39

A: Molecule type: mRNA
A: Residues: 1-117 <WAR>
A: Cross-references: UNIPARC:UPI0000115FFA; EMBL:X61651; NID:937731; PIDN:CAA43832.1; PID: F;15-98/Domain: immunoglobulin V region; immunoglobulin homology <IMM>

Query Match 100.0% Score 33; DB 2; Length 117;
Best Local Similarity 100.0%; **Pred.** No. 32;
Matches 5; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Qy 1 TYWIG 5
Db 31 TYWIG 35

A: Molecule type: mRNA
A: Residues: 1-119 <GRI>
A: Cross-references: UNIPARC:UPI00001180B9; EMBL:218848; NID:933122; PIDN:CAA79300.1; PID: F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0% Score 33; DB 2; Length 119;
Best Local Similarity 100.0%; **Pred.** No. 33;
Matches 5; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Qy 1 TYWIG 5
Db 31 TYWIG 35

A: Molecule type: mRNA
A: Residues: 1-127 <VAN>
A: Cross-references: UNIPARC:UPI0000176B99

A: Experimental source: PBMC
C: Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
C: Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0% Score 33; DB 2; Length 127;
Best Local Similarity 100.0%; **Pred.** No. 35;
Matches 5; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Qy 1 TYWIG 5
Db 31 TYWIG 35

A: Molecule type: mRNA
A: Residues: 1-127 <VAN>
A: Cross-references: UNIPARC:UPI0000176B99

A: Experimental source: PBMC
C: Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
C: Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0% Score 33; DB 2; Length 127;
Best Local Similarity 100.0%; **Pred.** No. 35;
Matches 5; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Qy 1 TYWIG 5
Db 31 TYWIG 35

A: Status: preliminary; nucleic acid sequence not shown

RESULT 8
 S57903 probable amino acid permease - *Lactobacillus delbrueckii* (fragment)
 C;Species: *Lactobacillus delbrueckii*
 C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 05-Oct-2004
 C;Accession: S57903
 R;Voncerichten, K.F.; Klein, J.R.; Matern, H.; Pleiss, R.
 M;Microbiology 140, 2591-2600, 1994
 A;Title: Cloning and nucleotide sequence analysis of *pepV*, a carnosinase gene from Lacto
 A;Reference number: S57902; MUID:95093606; PMID:7528082
 A;Accession: S57903
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-175 <VON>
 A;Cross-references: UNIPROT:P45495; UNIPARC:UPI000013BDC8; EMBL:231377; NID:g577568; PID:
 C;Genetics:
 A;Start codon: TTG
 C;Superfamily: ecotropic retrovirus receptor protein

RESULT 9
 P75561 hypothetical protein - *Deinococcus radiodurans* (strain R1)
 C;Species: *Deinococcus radiodurans*
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: F75561
 R;White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Ma
 s.M.; Shen, H.O.; Ventar, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A;Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A;Reference number: A75250; MUID:20036896; PMID:10567266
 A;Accession: F75561
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-181 <WHI>
 A;Cross-references: UNIPROT:Q9RY56; UNIPARC:UPI00000C16C8; GB:AE000513; NID:
 A;Experimental source: strain R1
 C;Genetics:
 A;Gene: DR0094
 A;Map position: 1

RESULT 10
 B84505 hypothetical protein At2g13130 [Imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear Cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
 C;Accession: B84505
 R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 Mi, Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Talton, L.
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A;Reference number: A84420; MUID:20083487; PMID:10617197

RESULT 11
 E71105 hypothetical protein PH0514 - *Pyrococcus horikoshii*
 C;Species: *Pyrococcus horikoshii*
 C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
 C;Accession: E71105
 R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hino, Y.; Yamamoto, S.; Sekir
 M.; Ohfuku, Y.; Punahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
 DNA Res. 5, 55-76, 1998
 A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
 A;Reference number: A71000; MUID:9834417; PMID:9679194
 A;Accession: E71105
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-32 <RAW>
 A;Cross-references: UNIPROT:058348; UNIPARC:UPI0000139B2F; GB:AP000003; NID:g3236130; PI
 A;Experimental source: strain OT3
 A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C;Genetics:
 A;Gene: PH0514

RESULT 12
 G75055 hypothetical protein PA0053 - *Pyrococcus abyssi* (strain Orsay)
 C;Species: *Pyrococcus abyssi*
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004
 C;Accession: G75055
 R;anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
 A;Reference number: A75001
 A;Accession: G75055
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-333 <RAW>
 A;Cross-references: UNIPROT:Q9YTS2; UNIPARC:UPI0000139BEC;
 A;Experimental source: strain Orsay
 C;Genetics:
 A;Gene: PAB0953
 C;Superfamily: hypothetical protein PYRAB14350 precursor
 Query Match Score 33; DB 2; Length 332;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TWIG 5
 Db 204 TWIG 208

RESULT 13
 G75055 hypothetical protein PA0053 - *Pyrococcus abyssi* (strain Orsay)
 C;Species: *Pyrococcus abyssi*
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004
 C;Accession: G75055
 R;anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
 A;Reference number: A75001
 A;Accession: G75055
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-333 <RAW>
 A;Cross-references: UNIPROT:Q9YTS2; UNIPARC:UPI0000139BEC;
 A;Experimental source: strain Orsay
 C;Genetics:
 A;Gene: PAB0953
 C;Superfamily: hypothetical protein PYRAB14350 precursor
 Query Match Score 33; DB 2; Length 333;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo.
A;Reference number: A95842; MUID:21396508; PMID:11481431

A;Accession: A95963
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-465 <KUR>
A;Cross-references: UNIPROT:UPI00000CB6FC; GB:AL591985; PIDN:CA49369.1;
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, P.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampo, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federpel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001.

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lealaure,
hebault, P.; Vandebab, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation
C;Genetics:
A;Gene: taud; SMB2529
A;Genome: plasmid

Query Match 100.0%; Score 33; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 1 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 314 TYWIG 318

Query Match 100.0%; Score 33; DB 2; Length 348;
Best Local Similarity 100.0%; Pred. No. 89; Matches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 36 TYWIG 40

Search completed: December 3, 2005, 14:33:34
Job time : 3.36735 secs

RESULT 14

D82186 beta-lactamase-related protein VC1562 [Imported] - Vibrio cholerae (strain N16961 serogroup O1) #Sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #Sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: D82186
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chadson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E.
L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: D82186
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-390 <HEI>
A;Cross-references: UNIPROT:Q9KRS4; UNIPARC:UPI00000C101A; GB:AB004233; GB:AE003852; MUID:21396508

C;Genetics:
A;Gene: VC1562
A;Map position: 1

Query Match 100.0%; Score 33; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 99; Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 100 TYWIG 104

RESULT 15
A95963 probable oxidoreductase protein taud [Imported] - Sinorhizobium meliloti (strain 1021) #Sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #Sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: A95963
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

Result No.	Query Score	Match Length	DB ID	Description
1	33	100.0	Q81053_DROME	Q8i53 drosophila
2	33	100.0	Q81CH9_DROME	Q8v1gh9 drosophila
3	33	100.0	Q9VRL1_DROME	Q9x125 drosophila
4	33	100.0	Q6X125_DROYA	Q9w1az2 oryza sativ
5	33	100.0	Q8WIA2_HUMAN	Q9udk8 homo sapien
6	33	100.0	Q9UDK8_HUMAN	P45495 lactobacill
7	33	100.0	YP6V_LACT	Q4mrvi bacillus ce
8	33	100.0	Q4NRV1_BACCE	Q6hdh2 bacillus th
9	33	100.0	Q6HDH2_BACCH	Q730i4 bacillus ce
10	33	100.0	Q730I4_BACCI	Q818B8 bacillus ce
11	33	100.0	Q818B8_BRCCR	Q811b9 entamoeba h
12	33	100.0	Q81LNS1_BRCCR	Q811ns1 entamoeba h
13	33	100.0	Q634U1_BACCCZ	Q634jj1 bacillus ce
14	33	100.0	Q9RY56_DEINOCOCCUS	Q9ry56 deinococcus
15	33	100.0	Q8C634_MOUSE	Q8C634 mus musculus
16	33	100.0	Q9ND13_ENTHI	Q9ndi3 entamoeba h
17	33	100.0	Q511T9_ENTHI	Q511t9 entamoeba h
18	33	100.0	Q4Q707_ENTHI	Q4qt07 entamoeba h
19	33	100.0	Q5EPGP4_ENTDI	Q5epgp4 entamoeba d
20	33	100.0	Q8A4JP6_ARATH	Q8ajp6 arabidopsis
21	33	100.0	Q8TDP9_HUMAN	Q8tdp9 homo sapien
22	33	100.0	Q8W189_ORYSA	Q8w189 oryza sativ
23	33	100.0	Q75XR6_EQUIUS	Q75xr6 equus cabal
24	33	100.0	Q67SS6_SYMTHE	Q67ss6 symbiobacter
25	33	100.0	Q9SUL5_ARATH	Q9sul5 arabidopsis
26	33	100.0	Y1614_PIRHO	Q58348 pyrococcus
27	33	100.0	Y1135_PIRAB	Q9uy82 pyrococcus
28	33	100.0	Q8U3H9_PYRFU	Q8u3h9 pyrococcus
29	33	100.0	Q554Z3_DICDI	Q554z3 dictyosteli
30	33	100.0	Q9PQ91_UREPA	Q9pq91 ureaplasma
31	33	100.0	Q4FQL5_9GAMM	Q4fq15 psychrobact

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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:11:48 ; Search time 8.81633 Seconds
 (without alignments)
 400.126 Million cell updates/sec

Title: US-10-769-144-13

Perfect score: 33

Sequence: 1 TWIG 5

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Database : UniProt 05.80.*
 Listing First 45 summaries

* 1: uniprot_sprot;*
 2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	33	100.0	Q81053_DROME	Q8i53 drosophila
2	33	100.0	Q81CH9_DROME	Q8v1gh9 drosophila
3	33	100.0	Q9VRL1_DROME	Q9x125 drosophila
4	33	100.0	Q6X125_DROYA	Q9udk8 oryza sativ
5	33	100.0	Q8WIA2_HUMAN	P45495 lactobacill
6	33	100.0	Q9UDK8_HUMAN	Q4mrvi bacillus ce
7	33	100.0	YP6V_LACT	Q6hdh2 bacillus th
8	33	100.0	Q4NRV1_BACCE	Q730i4 bacillus ce
9	33	100.0	Q6HDH2_BACCH	Q818B8 bacillus ce
10	33	100.0	Q730I4_BACCI	Q811b9 entamoeba h
11	33	100.0	Q818B8_BRCCR	Q811ns1 entamoeba h
12	33	100.0	Q81LNS1_BRCCR	Q811t9 entamoeba h
13	33	100.0	Q634U1_BACCCZ	Q634jj1 bacillus ce
14	33	100.0	Q9RY56_DEINOCOCCUS	Q9ry56 deinococcus
15	33	100.0	Q8C634_MOUSE	Q8C634 mus musculus
16	33	100.0	Q9ND13_ENTHI	Q9ndi3 entamoeba h
17	33	100.0	Q511T9_ENTHI	Q511t9 entamoeba h
18	33	100.0	Q4Q707_ENTHI	Q4qt07 entamoeba h
19	33	100.0	Q5EPGP4_ENTDI	Q5epgp4 entamoeba d
20	33	100.0	Q8A4JP6_ARATH	Q8ajp6 arabidopsis
21	33	100.0	Q8TDP9_HUMAN	Q8tdp9 homo sapien
22	33	100.0	Q8W189_ORYSA	Q8w189 oryza sativ
23	33	100.0	Q75XR6_EQUIUS	Q75xr6 equus cabal
24	33	100.0	Q67SS6_SYMTHE	Q67ss6 symbiobacter
25	33	100.0	Q9SUL5_ARATH	Q9sul5 arabidopsis
26	33	100.0	Y1614_PIRHO	Q58348 pyrococcus
27	33	100.0	Y1135_PIRAB	Q9uy82 pyrococcus
28	33	100.0	Q8U3H9_PYRFU	Q8u3h9 pyrococcus
29	33	100.0	Q554Z3_DICDI	Q554z3 dictyosteli
30	33	100.0	Q9PQ91_UREPA	Q9pq91 ureaplasma
31	33	100.0	Q4FQL5_9GAMM	Q4fq15 psychrobact

"The genome sequence of Drosophila melanogaster."

RL	Science 287:2185-2195 (2000).	
RP	NUCLEOTIDE SEQUENCE MEDLINE=22426055; PubMed=12537568;	[2]
RX	Celinker S.B., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champé M., Dugan S.P., Frise B., Hodgeson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Paclob J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.B., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence," Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).	
RN		[3]
RP	NUCLEOTIDE SEQUENCE MEDLINE=22426070; PubMed=12537573;	
RA	Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirkas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celinker S.B., "The transposable elements of the Drosophila melanogaster euchromatin: a genomic perspective," Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20 (2002).	
RN		[4]
RP	NUCLEOTIDE SEQUENCE MEDLINE=22426059; PubMed=12537572;	
RA	Misra S., Crosby M.A., Mungall C.J., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P., Bentzcouen R., Celinker S.B., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E., "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review," Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).	
RN		[5]
RP	NUCLEOTIDE SEQUENCE.	
RA	Berkeley Drosophila Genome Project, Celinker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R., Hoskins R., Stapleton M., Park S., Svirkas R., Smith E., Yu C., Rubin G., "Drosophila melanogaster release 4 sequence," Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	
RN		[6]
RP	NUCLEOTIDE SEQUENCE.	
RA	FlyBase ; Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.	
CC	-1 SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.	
DR	EMBL; AE003566; AN012119.1; -; Genomic_DNA.	
HSPP	Q15819; 177D.	
DR	Ensembl; CG10640; Drosophila melanogaster.	
DR	FlyBase ; FBgn0035601; UevIA.	
GO	GO:0004840; F:ubiquitin conjugating enzyme activity; IEA.	
GO	GO:0006512; P:ubiquitin cycle; IEA.	
DR	InterPro; IPR000608; 'UBQ-conjugat_E2'.	
PFAM	PF01079; UQ_conn_1.	
DR	ProDom; PD000461; UBQ_conn.	
DR	SMART; SM00212; 'UBQC_1'.	
DR	PROSITE; PS50127; 'UBIQUITIN_CONJUGAT_2'.	
FT	NON_TER 1	
SQ	SEQUENCE 137 AA; 15891 MW; 9ARC788A7F22EDC3 CRC64;	
Query Match	Score 33; DB 2; Length 137;	
Best Local Similarity	100.0%; Pred. No. 3e-02;	
Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 TYWIG 5	
DB	38 TYWIG 42	
RN		[1]
RP	NUCLEOTIDE SEQUENCE.	
RA	Medline=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celinker S.B., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scheer S.E., Li P.W., Hawkins R.A., Gallo R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H.C., Blazej R.G., Channe M., Name=UevIA; ORFNames=CG10640; Drosophila melanogaster (Fruit fly).	
RA	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.	
RA	NCBI_TaxID=7227;	
RN		[2]
RP	NUCLEOTIDE SEQUENCE.	
RA	Medline=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celinker S.B., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scheer S.E., Li P.W., Hawkins R.A., Gallo R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H.C., Blazej R.G., Channe M., Name=UevIA; ORFNames=CG10640; Drosophila melanogaster (Fruit fly).	
RA	Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,	

- | | |
|---|--|
| Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases. | |
| RL | RN [7] |
| RA | NUCLEOTIDE SEQUENCE. |
| RA | STRAIN=Berkeley; |
| RA | Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champ M., Chavez C., Dorsett V., Farfan D., Friis E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nuncio J., Pacie J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S. |
| RA | Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases. |
| RA | DR EMBL; AEG03566; AAIF50784.1; -; genomic_DNA. |
| RA | DR EMBL; AY06304; AAIF25423.1; -; mRNA. |
| RA | DR HSSP; P53152; 1 JAT. |
| RA | DR Ensemble; CG10640; Drosophila melanogaster. |
| RA | DR FlyBase; FBgn035601; CG10640. |
| RA | DR FlyBase; FBgn035601; Dev1A. |
| RA | DR GO; GO:0004840; Ubiquitin conjugation cycle; IEA. |
| RA | DR GO; GO:0006512; Ubiquitin cycle; IEA. |
| RA | DR InterPro; IPR00608; UBO-conjugat_E2. |
| RA | DR Pfam; PF00179; UQ.con; 1. |
| RA | DR PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1. |
| RA | DR SEQNCB; 145 AA; 16669 MW; BDF48A10486E0D8C CRC64; |
| RA | Query Match 100.0%; Score 33; DB 2; Length 145; |
| RA | Best Local Similarity 100.0%; Pred. No. 3.1e+02; |
| RA | Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| RA | Qy 1 TYWIG 5

Db 46 TYWIG 50 |
| RP | NUCLEOTIDE SEQUENCE. MEDLINE=22426065; PubMed=12557568; |
| RA | Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A., Patel S., Adams M., Chang M., Dugan S.P., Friis E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svartek R., Tabor P.B., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scheer S.E., Myers B.W., Gibbs R.A., Rubin G.M.; "Finishing a whole genome shotgun release 3 of the Drosophila melanogaster euchromatic genome sequence.", Genome Biol. 3:RESEARCH079-RESEARCH079 (2002). |
| RA | RT "The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective.", Genome Biol. 3:RESEARCH084.1-RESEARCH084.20 (2002). |
| RA | RT "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.", Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002). |
| RN | NUCLEOTIDE SEQUENCE. MEDLINE=22426070; PubMed=12557573; |
| RA | Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirska R., Patel S., Friis E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., Lewis S.E., Rubin G.M., "The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective.", Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20 (2002). |
| RN | NUCLEOTIDE SEQUENCE. MEDLINE=22426059; PubMed=12557572; |
| RA | Misra S., Crooky M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kainthaler R.S., Milligan G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Betreccourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.; "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.", Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002). |
| RT | Berkeley Drosophila Genome Project; Celinker S., Carlson J., Wan K., Prentiss B., Friis E., George R., Hoskins R., Stapleton M., Pacie J., Park S., Svirska R., Smith E., Yu C., Rubin G.; "Drosophila melanogaster release 4 sequence.", Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases. |
| RN | NUCLEOTIDE SEQUENCE. FlyBase. |

RC STRAIN=G9241;
 RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
 RA Hofmaster A.R., Ravel J., Rakko D.A., Chapman G.D., Chute M.D.,
 RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
 RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
 RA Rilstone J., Petersen S.N., Weyant R.S., Galloway D.R., Read T.D.,
 RA Popovic T., Fraser C.M.;
 RT "Identification of anthrax toxin genes in a *Bacillus cereus* associated
 with an illness resembling inhalation anthrax.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454 (2004).
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR EMBL; AE00100001; EAL14898.1; -; Genomic_DNA.
 KW Hypothetical protein;
 SQ SEQUENCE 178 AA; 20245 MW; 7335039A2DE9847A CRC64;
 Query Match 100.0%; Score 33; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TYWIG 5
 Db 32 TYWIG 36

RESULT 9
 Q6HDH2_BACHK
 ID Q6HDH2_BACHK PRELIMINARY;
 AC Q6HDH2;
 DT 05-JUL-2004 ("TREMBLrel. 27, Created")
 DT 05-JUL-2004 ("TREMBLrel. 27, Last sequence update")
 DT 05-JUL-2004 ("TREMBLrel. 27, Last annotation update")
 DE Hypothetical protein.
 OrderedLocusNames=BAC4347;
 GN Bacillus cereus (strain ATCC 14579 / DSM 31).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 NCBI_TaxID=229900;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
 RA Ivanova N., Sorokin A., Anderson K., Galleron N., Canuelon B.,
 RA Kapitral V., Bhattacharyya A., Resnik G., Mikhailova N., Lapidus A.,
 RA Chu L., Mazur M., Gotsman E., Larsen N., D'Souza M., Walunas T.,
 RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
 RA Overbeek R., Kyprides N.C.;
 RT "Genome sequence of *Bacillus cereus* and comparative analysis with
Bacillus anthracis";
 RL Nature 423:87-91 (2003).
 DR EMBL; AB017012; AAP11260.1; -; Genomic_DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 178 AA; 20384 MW; 0EA5R67C129A1802 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TYWIG 5
 Db 32 TYWIG 36

RESULT 10
 Q73014_BACCI
 ID Q73014_BACCI PRELIMINARY;
 AC Q73014;
 DT 05-JUL-2004 ("TREMBLrel. 27, Created")
 DT 05-JUL-2004 ("TREMBLrel. 27, Last sequence update")
 DT 05-JUL-2004 ("TREMBLrel. 27, Last annotation update")
 DE Hypothetical protein.
 OrderedLocusNames=BCB4432;
 GN Bacillus cereus (strain ATCC 10987).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 NCBI_TaxID=222523;

RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=1496074; DOI=10.1093/nar/gkh258;
 RA Raskin D.A., Ravel J., Oekstad O.A., Halgason E., Cer R.Z., Jiang L.,
 RA Shores K.A., Pouts D.E., Tourrasse N.J., Anguilo S.V., Kolonay J.F.,
 RA Nelson W.C., Kolstoe A.B., Fraser C.M., Read T.D.;
 RT "The genome sequence of *Bacillus cereus* ATCC 10987 reveals metabolic
 adaptations and a large plasmid related to *Bacillus anthracis* pXO1.";
 RL Nucleic Acids Res. 32:97-988 (2004).
 DR EMBL; AE017277; AAS43333.1; -; Genomic_DNA.
 DR TIGR; BCB4432; -;
 KW Complete proteome.
 SQ SEQUENCE 178 AA; 20187 MW; A4R6PCBBB6E51192 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
 Q81858_BACCR
 ID Q81858_BACCR PRELIMINARY;
 AC Q81858;
 DT 01-JUN-2003 ("TREMBLrel. 24, Created")
 DT 01-JUN-2003 ("TREMBLrel. 24, Last sequence update")
 DT 01-JUN-2003 ("TREMBLrel. 24, Last annotation update")
 DE Hypothetical protein.
 OrderedLocusNames=BC4347;
 OS Bacillus cereus (strain ATCC 14579 / DSM 31).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 NCBI_TaxID=229900;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
 RA Ivanova N., Sorokin A., Anderson K., Galleron N., Canuelon B.,
 RA Kapitral V., Bhattacharyya A., Resnik G., Mikhailova N., Lapidus A.,
 RA Chu L., Mazur M., Gotsman E., Larsen N., D'Souza M., Walunas T.,
 RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
 RA Overbeek R., Kyprides N.C.;
 RT "Genome sequence of *Bacillus cereus* and comparative analysis with
Bacillus anthracis";
 RL Nature 423:87-91 (2003).
 DR EMBL; AB017012; AAP11260.1; -; Genomic_DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 178 AA; 20184 MW; 66ZAC78BF69F1489 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
 Q81LNS_BACAN
 ID Q81LNS_BACAN PRELIMINARY;
 AC Q81LNS;
 DT 01-JUN-2003 ("TREMBLrel. 24, Created")
 DT 01-JUN-2003 ("TREMBLrel. 24, Last sequence update")
 DT 10-MAY-2005 ("TREMBLrel. 30, Last annotation update")
 DE Hypothetical protein.
 OrderedLocusNames=BAC4579;
 OS Bacillus anthracis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 NCBI_TaxID=1392;

Qy 1 TYWIG 5
 Db 32 TYWIG 36

RN	[1]	SQ	SEQUENCE	178 AA;	Score 33; DB 2; Length 178;	
RP	NUCLEOTIDE SEQUENCE.					
RC	STRAIN="Ames / 180L"e Porton;					
RX	MEDLINE=2260814; PubMed=1271629; DOI=10.1038/nature01586;					
RA	Read T.D., Peterson S.N., Tourasse N.J., Ballie L.W., Paulsen I.T.,					
RA	Nelson K.B., Tettelin H., Routs D.E., Eisen J.A., Gill S.R.,					
RA	Holzapfel E.K., Oksstad O.A., Heiglason S., Rilstone J., Wu M.,					
RA	Kolonay J.F., Beaman M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,					
RA	DeBoy R.T., Madupu R., Daugherty S.C., Durkin A.S., Haft D.H.,					
RA	Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,					
RA	Bentton J.U., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,					
RA	Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nieman W.C.,					
RA	Hazen A., Cline R.T., Redmond C., Thwaite J.B., White O.,					
RA	Hanna P.C., Molstoe A.-B., Fraser C.M., Friedlander A.M., Koehler T.M.,					
RA	"The genome sequence of <i>Bacillus anthracis</i> Ames and comparison to closely related bacteria.";					
RT	RT					
RL	Nature 423:81-86 (2003).					
RN	[2]	SQ	SEQUENCE.			
RC	STRAIN="Ames / 180L"e 0581;					
RA	Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,					
RA	Wilson M., Stanley S., Decker S., Read T.D., Salterberg S.L.,					
RA	Frazer C.M.,					
RT	" <i>Bacillus anthracis</i> comparative genomics.";					
RL	Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.					
RN	[3]	SQ	SEQUENCE [LARGE SCALE GENOMIC DNA].			
RP	NUCLEOTIDE SEQUENCE [STEREOLYSESERINE]					
RC	STRAIN="Sterne"					
RA	Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,					
RA	Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,					
RA	Richardson P., Rubin E., Tice H.;					
RT	"Complete genome sequence of <i>Bacillus anthracis</i> Sterne."					
RT	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.					
RL	DR	DR	DR			
DR	AEO17038; AE028286.1; -; Genomic DNA.					
DR	EMBL; AE017334; AE033699.1; -; Genomic DNA.					
DR	EMBL; AE017225; AE056547.1; -; Genomic DNA.					
DR	TIGR; BA1579; -.					
DR	DR	DR	DR			
KW	Complete proteome; Hypothetical protein.					
SQ	SEQUENCE 178 AA; 20212 MW; 73C86BC8583764C CRC64;					
Query Match	100.0%; Score 33; DB 2; Length 178;					
Best Local Similarity	100.0%; Pred. No. 3.8e+02;					
Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	[1] TYWIG 5					
Db	32 TYWIG 36					
RESULT 13						
ID	Q634J1_BACZZ	PRELIMINARY;	PRT;	178 AA.		
AC	Q634J1;					
DT	25-OCT-2004 (TREMBLrel. 28, Created)					
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)					
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)					
DN	HYPOTHETICAL PROTEIN.					
GN	ORPNames=BCE3314097.					
OS	<i>Bacillus cereus</i> (strain ZK)					
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; <i>Bacillus</i> ; <i>Bacillus cereus</i> group.					
OC	NCBI_TaxID=288881;					
RN	[1]	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].				
RP	Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,					
RA	Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,					
RA	Richardson P., Rubin E., Tice H.;					
RT	"Complete genome sequence of <i>Bacillus cereus</i> ZK."					
RT	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.					
DR	EMBL; CP000001; AUU16170.1; -; Genomic DNA.					
KW	Complete proteome; Hypothetical protein.					
RESULT 14						
ID	Q8C634_MOUSE	PRELIMINARY;	PRT;	189 AA.		
AC	Q8C634;					
DT	01-MAR-2003 (TREMBLrel. 23, Created)					
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)					
DT	01-MAR-2005 (TREMBLrel. 30, Last annotation update)					
DE	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:492:502D1 product: hypothetical C-type lectin domain containing protein, full insert sequence (similar to C lectin-related protein AI).					
DE	NCBI_TaxID=10990;					
GN	Name=492:502D1Rik;					
GN	Mus musculus (Mouse).					
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;					
OC	Muroidea; Muridae; Murinae; Mus.					
RN	[1]	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=C57BL/6J; TISSUE=Testis;					

- RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RX Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning.";
 RT Meth. Enzymol. 303:19-44(1999).
 RL [2]
- RX NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=Testis;
 MEDLINE=2:108566; PubMed=11217851; DOI=10.1038/35055500;
 Kawai J., Shinagawa A., Shikata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fujikuda S.,
 Aizawa K., Izakazi Y., Nishi K., Kiyoysawa H., Kondo S., Yamamoto I.,
 Saito T., Okazaki Y., Gotojori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 Fleischmann W., Gaasterland T., Gibbs C., King B., Kochiwa H.,
 Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
 Blake J., O'Keffe D., Botunga N., Carninci P., de Bonalde M.F.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M.,
 Gustincich S., Hill D., Hofmann D.A., Kaniya M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzairelli J., Mombarts P.,
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 Suzuki H., Toyoo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 Wynnshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
- RX NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=Testis;
 MEDLINE=2:2354683; PubMed=146651; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamamoto I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbett L.B., Cousins S.,
 RA Dalla B., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
 RA Gaasterland T., Garibaldi M., Gissi C., Godzik A., Gough J.,
 RA Grimond S., Gustincich S., Hirokawa N., Jackson R.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Magioli D.R., Maltais L., Brusic V., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perera G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultan R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynnshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 RN [4]
- RX NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=Testis;
 MEDLINE=20499374; PubMed=1042159; DOI=10.1101/gr.145100;
 RX Carninci P., Shikata Y., Hayatsu N., Sugahara Y., Shikata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalisation and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 RN [5]
- RX NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=Testis;
 RN [6]
- RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152660;
 RA Shikata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Tashiro H., Itoh M.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujikawa S., Inoue K., Togawa Y., Izawa M., Ohara B., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RA "Riken integrated (RISA) system-384-format sequencing pipeline with 384 multi-capillary sequencer.";
 RL Genome Res. 10:1757-1771 (2000).
 RN [7]
- RX NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Aizawa K., Akimura T., Bono H., Carninci P.,
 RA Fukiuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Fukuhida K., Hayatsu N., Hiramoto K., Hirako T., Hirono T.,
 RA Horii R., Imotani K., Ishii Y., Itoh M., Kagawa I., Kurokawa T.,
 RA Katch H., Kawai J., Koijima Y., Kondo S., Kono H., Koda M., Koya S.,
 RA Kohihara C., Matsuyama T., Miyazaki A., Murat M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki N.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi T., Tomaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toda T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RA Submitted (APR-2002) to the EMBL/GenBank/DBBJ databases.
 RL Submitted (APR-2002) to the EMBL/GenBank/DBBJ databases.
 RN [8]
- RX NUCLEOTIDE SEQUENCE.
 TISSUE=Testis;
 MEDLINE=22388227; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX TISSUE=Testis;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shamen C.M., Schulier G.D.,
 RA Altenschul S.F., Zeeberg B., Buettow K.R., Schefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina A.A., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Logquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalob D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grifith J., Schmitz J., Myers R.N.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialow D.E.,
 RA Scheraga A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [8]
- RX NUCLEOTIDE SEQUENCE.
 TISSUE=Testis;
 Director MGC Project; to the EMBL/GenBank/DBBJ databases.
 DR Submitted (FEB-2005) to the EMBL/GenBank/DBBJ databases.
 DR EMBL; AK076635; BAC6425.1; - ; mRNA.
 DR EMBL; BC083479; AAH9479.1; - ; mRNA.
 DR Ensemble: ENSMUSG0000047720; Mus musculus.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR InterPro: IPR001304; Lectin_C.
 DR Pfam; PF00059; Lectin_C_1.
 DR SMART; SM00034; CLECT_1.
 DR PROSITE; PS50014; C_TYPE_LECTIN_2_1.
 DR Hypothetical protein; Lectin.
 KW SEQUENCE 189 AA; 22107 MW; 2E8573DBAC2B39E CRC64;
- Query Match Score 33; DB 2; Length 189;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
- QY 1 TYWIG 5 |||||

Db 127 TYWIG 131

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Job time : 11.8163 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:24:58 ; Search time 2.12245 Seconds
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Title: US-10-769-144-13
 Perfect score: 33
 Sequence: 1 TWIG 5

Scoring table: BLASTM62
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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

RESULT 1
 US-09-726-219A-172
 ; Sequence 172, Application US/09726219A
 ; Patent No. 6806079

GENERAL INFORMATION:

/ APPLICANT: Cambridge Antibody Technology Limited
 / APPLICANT: Cambridge Antibody Technology Limited
 / APPLICANT: Medical Research Council
 / APPLICANT: McCafferty, John
 / APPLICANT: Pope, Anthony
 / APPLICANT: Johnson, Kevin
 / APPLICANT: Hoogenboom, Hendricus
 / APPLICANT: Griffiths, Andrew
 / APPLICANT: Jackson, Ronald
 / APPLICANT: Holliger, Kasper
 / APPLICANT: Marks, James
 / APPLICANT: Clackson, Timothy
 / APPLICANT: Chiawell, David
 / APPLICANT: Winter, Gregory
 / APPLICANT: Bonert, Timothy
 / APPLICANT: Methods for Producing Members of Specific Binding Pairs
 / FILE REFERENCE: 213833-0013
 / CURRENT APPLICATION NUMBER: US/09/726,219A
 / CURRENT FILING DATE: 2000-11-28
 / PRIOR APPLICATION NUMBER: GB 9015198.6
 / PRIOR FILING DATE: 1990-07-10
 / PRIOR APPLICATION NUMBER: GB 9022845.3
 / PRIOR FILING DATE: 1990-10-19
 / PRIOR APPLICATION NUMBER: GB 9022845.3
 / PRIOR FILING DATE: 1990-10-19
 / PRIOR APPLICATION NUMBER: GB 9024503.6
 / PRIOR FILING DATE: 1990-11-12
 / PRIOR APPLICATION NUMBER: GB 9104744.9
 / PRIOR FILING DATE: 1991-03-06
 / PRIOR APPLICATION NUMBER: GB 9110549.4
 / PRIOR FILING DATE: 1991-05-15
 / PRIOR APPLICATION NUMBER: PCT/GB91/01134
 / PRIOR FILING DATE: 1991-07-10
 / PRIOR APPLICATION NUMBER: US 07/971,857
 / PRIOR FILING DATE: 1993-01-08
 / LENGTH: 88
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-09-726-219A-172

ALIGNMENTS

Issued Patents AA:
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 3: /cgn2_6/podata/1/iaa/H_COMB.pep:
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 No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	33	100.0	88	2 US-09-726-219A-172
2	33	100.0	88	2 US-09-196-512-172
3	33	100.0	151	2 US-09-270-767-44527
4	33	100.0	430	2 US-09-328-535-5453
5	32	97.0	383	2 US-09-902-540-11130
6	32	97.0	415	2 US-09-202-510-9936
7	31	97.0	616	2 US-09-540-216-3084
8	31	93.9	5	2 US-09-210-262A-1
9	31	93.9	110	2 US-09-252-991A-10248
10	31	93.9	119	2 US-09-262A-7
11	31	93.9	315	2 US-09-903-208A-212
12	31	93.9	483	2 US-09-208A-210
13	31	93.9	484	2 US-09-328-352-4849
14	31	93.9	488	2 US-09-228-352-4928
15	30	90.9	476	2 US-09-328-352-5950
16	29	87.9	8	2 US-08-444-818-602
17	29	87.9	8	2 US-08-444-818-603
18	29	87.9	8	2 US-08-444-818-604
19	29	87.9	98	1 US-08-471-039-81
20	29	87.9	98	1 US-08-176-342A-81
21	29	87.9	98	1 US-08-665-202-33
22	29	87.9	98	2 US-10-194-975-45
23	29	87.9	98	2 US-09-515-697-133
24	29	87.9	117	2 US-09-515-697-133
25	29	87.9	117	2 US-09-769B-26
26	29	87.9	119	2 US-09-025-769B-26
27	29	87.9	119	2 US-09-490-153-26
28	29	87.9	119	2 US-09-490-324-26
29	29	87.9	120	2 US-09-025-769B-67
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31	29	87.9	120	2 US-09-490-070A-40
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33	29	87.9	120	2 US-09-490-153-67
34	29	87.9	120	2 US-09-490-153-67
35	29	87.9	120	2 US-09-490-153-67
36	29	87.9	120	2 US-09-490-153-67
37	29	87.9	120	2 US-09-490-324-67
38	29	87.9	121	1 US-08-388-672A-20
39	29	87.9	121	1 US-08-388-672A-23
40	29	87.9	122	2 US-09-080-554-23
41	29	87.9	122	2 US-08-983-607-30
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43	29	87.9	131	2 US-09-291-522-6
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45	29	87.9	193	2 US-09-543-681A-4479

Query Match Best Local Similarity 100.0%; Score 33; DB 2; Length 88;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
 Db 31 TYWIG 35

RESULT 2
 US-09-196-522-172
 / Sequence 172, Application US/09196522

/ Patent No. 6916605

/ GENERAL INFORMATION:

/ APPLICANT: Cambridge Antibody Technology Limited

/ APPLICANT: Cambridge Antibody Technology Council

/ APPLICANT: Medical Research Council

/ APPLICANT: McCafferty, John

/ APPLICANT: Pope, Anthony

/ APPLICANT: Johnson, Kevin

/ APPLICANT: Hoogenboom, Hendrikus

/ APPLICANT: Griffitns, Andrew

/ APPLICANT: Jackson, Ronald

/ APPLICANT: Holliger, Kasper

/ APPLICANT: Marks, James

/ APPLICANT: Clackson, Timothy

/ APPLICANT: Chiswell, David

/ APPLICANT: Winter, Gregory

/ APPLICANT: Bonert, Timothy

/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs

/ FILE REFERENCE: 213839-00004

/ CURRENT APPLICATION NUMBER: US/09/196,522

/ CURRENT FILING DATE: 1998-11-28

/ PRIOR APPLICATION NUMBER: GB 9015198.6

/ PRIOR FILING DATE: 1990-07-10

/ PRIOR APPLICATION NUMBER: GB 9022845.3

/ PRIOR FILING DATE: 1990-10-19

/ PRIOR APPLICATION NUMBER: GB 9022845.3

/ PRIOR FILING DATE: 1990-10-19

/ PRIOR APPLICATION NUMBER: GB 9024503.6

/ PRIOR FILING DATE: 1990-11-12

/ PRIOR APPLICATION NUMBER: GB 9104744.9

/ PRIOR FILING DATE: 1991-03-06

/ PRIOR APPLICATION NUMBER: GB 9110549.4

/ PRIOR FILING DATE: 1991-05-15

/ PRIOR APPLICATION NUMBER: PCT/GB91/01134

/ PRIOR FILING DATE: 1991-07-10

/ PRIOR APPLICATION NUMBER: US 07/971,857

/ PRIOR FILING DATE: 1993-01-08

/ NUMBER OF SEQ ID NOS: 272

/ SOFTWARE: PatentIn version 3.1

/ SEQ ID NO: 172

/ LENGTH: 88

/ ORGANISM: Homo sapiens

/ US-09-196-522-172

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/ Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/ SEQ ID NO: 172

/ TYPE: PRT

/ ORGANISM: Myxococcus xanthus

/ US-09-902-540-11130

/ Query Match Best Local Similarity 100.0%; Score 33; DB 2; Length 88;

/ Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/ SEQ ID NO: 11130

/ TYPE: PRT

/ ORGANISM: Myxococcus xanthus

/ US-09-902-540-11130

RESULT 3
 US-09-270-767-44527

/ Sequence 44527, Application US/09270767

/ Patent No. 6703491

/ GENERAL INFORMATION:

/ APPLICANT: Homburger et al. / TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster* / FILE REFERENCE: File Reference: 7126-094 / CURRENT APPLICATION NUMBER: US/09/270,767 / CURRENT FILING DATE: 1999-03-17 / NUMBER OF SEQ ID NOS: 62517 / SOFTWARE: PatentIn Ver. 2.0 / SEQ ID NO: 44527 / LENGTH: 151 / TYPE: PRT / ORGANISM: *Drosophila melanogaster* / US-09-270-767-44527/

/ Query Match Best Local Similarity 100.0%; Score 33; DB 2; Length 151;

/ Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/ SEQ ID NO: 44527

/ TYPE: PRT

/ ORGANISM: *Drosophila melanogaster*

RESULT 4
 US-09-328-352-5453

/ Sequence 5453, Application US/09328352

/ Patent No. 6562958

/ GENERAL INFORMATION:

/ APPLICANT: Gary L. Breton et al. / TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER / FILE REFERENCE: GTC9-03PA / CURRENT APPLICATION NUMBER: US/09/328,352 / CURRENT FILING DATE: 1999-06-04 / NUMBER OF SEQ ID NOS: 8252 / SEQ ID NO: 5453 / LENGTH: 430 / TYPE: PRT / ORGANISM: *Acinetobacter baumannii* / US-09-328-352-5453

/ Query Match Best Local Similarity 100.0%; Score 33; DB 2; Length 430;

/ Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/ SEQ ID NO: 5453

/ TYPE: PRT

/ ORGANISM: *Acinetobacter baumannii*

RESULT 5
 US-09-902-540-11130

/ Sequence 11130, Application US/09902540

/ Patent No. 6833447

/ GENERAL INFORMATION:

/ APPLICANT: Goldinan, Barry S. / APPLICANT: Hinke, Gregory J. / APPLICANT: Slater, Steven C. / APPLICANT: Wiegand, Roger C. / TITLE OF INVENTION: *Myxococcus xanthus* Genome Sequences and Uses Thereof / FILE REFERENCE: 38-10(15849)B / CURRENT APPLICATION NUMBER: US/09/902,540 / CURRENT FILING DATE: 2000-07-10 / NUMBER OF SEQ ID NOS: 16825 / SEQ ID NO: 11130 / LENGTH: 383 / TYPE: PRT

/ Query Match Best Local Similarity 100.0%; Score 32; DB 2; Length 383;

/ Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/ SEQ ID NO: 11130

/ TYPE: PRT

/ ORGANISM: *Myxococcus xanthus*

RESULT 6
 US-09-902-540-11130

/ Sequence 11130, Application US/09902540

/ Patent No. 6833447

/ GENERAL INFORMATION:

/ APPLICANT: Goldinan, Barry S. / APPLICANT: Hinke, Gregory J. / APPLICANT: Slater, Steven C. / APPLICANT: Wiegand, Roger C. / TITLE OF INVENTION: *Myxococcus xanthus* Genome Sequences and Uses Thereof / FILE REFERENCE: 38-10(15849)B / CURRENT APPLICATION NUMBER: US/09/902,540 / CURRENT FILING DATE: 2000-07-10 / NUMBER OF SEQ ID NOS: 16825 / SEQ ID NO: 11130 / LENGTH: 383 / TYPE: PRT

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/ Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/ SEQ ID NO: 11130

/ TYPE: PRT

/ ORGANISM: *Myxococcus xanthus*

RESULT 7
 US-09-902-540-11130

/ Sequence 11130, Application US/09902540

/ Patent No. 6833447

/ GENERAL INFORMATION:

/ APPLICANT: Goldinan, Barry S. / APPLICANT: Hinke, Gregory J. / APPLICANT: Slater, Steven C. / APPLICANT: Wiegand, Roger C. / TITLE OF INVENTION: *Myxococcus xanthus* Genome Sequences and Uses Thereof / FILE REFERENCE: 38-10(15849)B / CURRENT APPLICATION NUMBER: US/09/902,540 / CURRENT FILING DATE: 2000-07-10 / NUMBER OF SEQ ID NOS: 16825 / SEQ ID NO: 11130 / LENGTH: 383 / TYPE: PRT

/ Query Match Best Local Similarity 100.0%; Score 32; DB 2; Length 383;

/ Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/ SEQ ID NO: 11130

/ TYPE: PRT

/ ORGANISM: *Myxococcus xanthus*

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Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TYWIG 5
Db 295 TYWVG 299

RESULT 6
US-09-902-540-9936 Application US/09902540
; Sequence 9336, Application US/09902540
; Patent No. 6833347
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-1011589.B
; CURRENT APPLICATION NUMBER: US/09/903,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16823
; SEQ ID NO: 9936
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; US-09-902-540-9936

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Best Local Similarity 80.0%; Pred. No. 3.7e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 58 TYWVG 62

RESULT 7
US-09-540-236-3084 Application US/09540236
; Sequence 3084, Application US/09540236
; Patent No. 6613910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACIDS AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; FILE REFERENCE: 2709 2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO: 3084
; LENGTH: 616
; TYPE: PRT
; ORGANISM: M.catarrhalis
; US-09-540-236-3084

Query Match Score 97.0%; Score 32; DB 2; Length 616;
Best Local Similarity 80.0%; Pred. No. 5.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
US-09-920-262A-1 Application US/09920262A
; Sequence 1, Application US/09920262A
; Patent No. 6902734
; GENERAL INFORMATION:
; APPLICANT: Shealy, David
; APPLICANT: Knight, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Peritt, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: CBN0248
; CURRENT FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,827
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO: 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-920-262A-1

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Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 1 TYWLG 5

RESULT 9
US-09-252-991A-18248 Application US/09252991A
; Sequence 18248, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 10196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 18248
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-18248

Query Match Score 93.9%; Score 31; DB 2; Length 110;
Best Local Similarity 80.0%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 85 TYWLG 89

RESULT 10
US-09-920-262A-7 Application US/09920262A
; Sequence 7, Application US/09920262A
; Patent No. 6902734
; GENERAL INFORMATION:
; APPLICANT: Shealy, David
; APPLICANT: Knight, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Peritt, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358
; CURRENT FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,827
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO: 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-920-262A-7
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|||:
Db 129 TYWIG 133

PRIOR FILING DATE: 2000-08-07
 PRIOR APPLICATION NUMBER: 60/236,827
 PRIOR FILING DATE: 2000-09-29
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: PatentIn Ver 3.1
 SEQ ID NO: 7
 LENGTH: 119
 TYPE: PRT
 ORGANISM: Homo sapiens
US-09-920-262A-7

Query Match 93.9%; Score 31; DB 2; Length 119;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
 Db 31 TYWIG 35

RESULT 11
US-09-603-208A-212
 Sequence 212, Application US/09603208A
 Patent No. 6822084

GENERAL INFORMATION:
 APPLICANT: Pompejus, Markus
 APPLICANT: Kroger, Burkhard
 APPLICANT: Schroder, Harwig
 APPLICANT: Zeider, Oskar
 APPLICANT: Haberhauer, Gregor
 APPLICANT: Lee, Heung-Shick
 APPLICANT: Kim, Hyung-Joon

TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS, RESISTANCE AND TOLERANCE PROTEINS
 FILE REFERENCE: BGI-124CP
 CURRENT APPLICATION NUMBER: US/09/603, 208A
 CURRENT FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: 60/141031
 PRIOR FILING DATE: 1999-06-23
 PRIOR APPLICATION NUMBER: 60/142692
 PRIOR FILING DATE: 1999-07-01
 PRIOR APPLICATION NUMBER: 60/151214
 PRIOR FILING DATE: 1999-08-27
 PRIOR APPLICATION NUMBER: DE 19930429.7
 PRIOR FILING DATE: 1999-07-01
 PRIOR APPLICATION NUMBER: DE 19931413.6
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19931457.8
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19931541.8
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19932209.0
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19932230.9
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19932914.1
 PRIOR FILING DATE: 1999-07-14
 PRIOR APPLICATION NUMBER: DE 19940764.9
 PRIOR FILING DATE: 1999-08-27
 PRIOR APPLICATION NUMBER: DE 19941382.7
 PRIOR FILING DATE: 1999-08-31
 NUMBER OF SEQ ID NOS: 306
 SEQ ID NO: 210
 LENGTH: 483
 TYPE: PRT
 ORGANISM: Corynebacterium glutamicum
US-09-603-208A-210

Query Match 93.9%; Score 31; DB 2; Length 483;
 Best Local Similarity 80.0%; Pred. No. 6.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
 Db 129 TYWIG 133

RESULT 12
US-09-603-208A-210
 Sequence 210, Application US/09603208A
 Patent No. 6822084

GENERAL INFORMATION:
 APPLICANT: Pompejus, Markus
 APPLICANT: Kroger, Burkhard
 APPLICANT: Schroder, Harwig
 APPLICANT: Zeider, Oskar
 APPLICANT: Haberhauer, Gregor
 APPLICANT: Lee, Heung-Shick
 APPLICANT: Kim, Hyung-Joon

TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS, RESISTANCE AND TOLERANCE PROTEINS
 FILE REFERENCE: BGI-124CP
 CURRENT APPLICATION NUMBER: US/09/603, 208A
 CURRENT FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: 60/141031
 PRIOR FILING DATE: 1999-06-23
 PRIOR APPLICATION NUMBER: 60/142692
 PRIOR FILING DATE: 1999-07-01
 PRIOR APPLICATION NUMBER: 60/151214
 PRIOR FILING DATE: 1999-08-27
 PRIOR APPLICATION NUMBER: DE 19930429.7
 PRIOR FILING DATE: 1999-07-01
 PRIOR APPLICATION NUMBER: DE 19931413.6
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19931457.8
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19931541.8
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19932209.0
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19932230.9
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19932914.1
 PRIOR FILING DATE: 1999-07-14
 PRIOR APPLICATION NUMBER: DE 19940764.9
 PRIOR FILING DATE: 1999-08-27
 PRIOR APPLICATION NUMBER: DE 19941382.7
 PRIOR FILING DATE: 1999-08-31
 NUMBER OF SEQ ID NOS: 306
 SEQ ID NO: 210
 LENGTH: 483
 TYPE: PRT
 ORGANISM: Corynebacterium glutamicum
US-09-603-208A-212

Query Match 93.9%; Score 31; DB 2; Length 315;
 Best Local Similarity 80.0%; Pred. No. 4.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5

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; SEQ ID NO: 4849
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4849

Query Match      93.9%;  Score 31;  DB 2;  Length 484;
Best Local Similarity 80.0%;  Pred. No. 6.4e+02;  Indels 0;  Gaps 0;
Matches 4;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 TWIG 5
      |||:
Db      111 TYWLG 115

RESULT 14
US-09-328-352-4928
; Sequence 4928, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTCC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO: 4928
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4928

Query Match      93.9%;  Score 31;  DB 2;  Length 488;
Best Local Similarity 80.0%;  Pred. No. 6.5e+02;  Indels 0;  Gaps 0;
Matches 4;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 TWIG 5
      |||:
Db      112 TYWLG 116

RESULT 15
US-09-328-352-5950
; Sequence 5950, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTCC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO: 5950
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5950

Query Match      90.9%;  Score 30;  DB 2;  Length 476;
Best Local Similarity 80.0%;  Pred. No. 9.5e+02;  Indels 0;  Gaps 0;
Matches 4;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 TWIG 5
      |||:
Db      257 TYWLG 261

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OM protein - protein search, using SW model

Run on: December 3, 2005, 13:27:13 ; Search time 6.85714 Seconds
 (without alignments)
 304.667 Million cell updates/sec

Title: US-10-769-144-13

Perfect score: 33

Sequence: 1 TYWIG 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	TYWIG 5	100.0	5	4	US-10-374-932-5	Sequence 5, Appli
2	TYWIG 5	100.0	5	4	US-10-379-741-5	Sequence 5, Appli
3	TYWIG 5	100.0	5	5	US-10-369-144-13	Sequence 13, Appli
4	TYWIG 5	100.0	5	5	US-10-851-658-92	Sequence 92, Appli
5	TYWIG 5	100.0	5	5	US-10-922-725-5	Sequence 5, Appli
6	TYWIG 5	100.0	5	5	US-10-903-191-13	Sequence 13, Appli
7	TYWIG 5	100.0	76	4	US-10-437-963-106931	Sequence 106931, Appli
8	TYWIG 5	100.0	88	4	US-10-853-622-172	Sequence 172, Appli
9	TYWIG 5	100.0	88	4	US-10-803-653-172	Sequence 172, Appli
10	TYWIG 5	100.0	116	3	US-10-851-614-4	Sequence 4, Appli
11	TYWIG 5	100.0	116	4	US-10-354-637-4	Sequence 4, Appli
12	TYWIG 5	100.0	116	5	US-10-769-144-4	Sequence 4, Appli
13	TYWIG 5	100.0	116	5	US-10-903-191-4	Sequence 4, Appli
14	TYWIG 5	100.0	125	5	US-10-891-658-79	Sequence 79, Appli
15	TYWIG 5	100.0	130	4	US-10-226-615-2	Sequence 2, Appli
16	TYWIG 5	100.0	130	4	US-10-374-932-2	Sequence 2, Appli
17	TYWIG 5	100.0	130	4	US-10-319-741-2	Sequence 2, Appli
18	TYWIG 5	100.0	130	5	US-10-982-725-2	Sequence 2, Appli
19	TYWIG 5	100.0	145	6	US-11-091-143-2335	Sequence 2335, Appli
20	TYWIG 5	100.0	248	3	US-09-880-748-1	Sequence 1, Appli
21	TYWIG 5	100.0	248	4	US-10-293-418-1	Sequence 1, Appli
22	TYWIG 5	100.0	373	4	US-10-270-92	Sequence 92, Appli
23	TYWIG 5	100.0	393	4	US-10-455-115-208389	Sequence 208389, Appli
24	TYWIG 5	100.0	411	5	US-10-769-144-12	Sequence 12, Appli
25	TYWIG 5	100.0	411	5	US-10-903-191-12	Sequence 12, Appli
26	TYWIG 5	100.0	468	5	US-10-769-144-2	Sequence 2, Appli
27	TYWIG 5	100.0	468	5	US-10-903-191-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
 US-10-374-932-5
 ; Sequence 5, Application US/10374932
 ; Publication No. US20050235586A1
 ; GENERAL INFORMATION:
 ; APPLICANT: van de Winkel, Jan G.J.
 ; APPLICANT: van Dijk, Marcus Antonius
 ; APPLICANT: Schuurman, Janine
 ; APPLICANT: Gerritsen, Arnout F.
 ; APPLICANT: Baadsgaard, Ole
 ; APPLICANT: Petersen, Jorgen
 ; TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)
 ; FILE REFERENCE: GMI -024CP
 ; CURRENT APPLICATION NUMBER: US/10/374,932
 ; PRIORITY APPLICATION NUMBER: US 60/314,731
 ; PRIOR FILING DATE: 2001-08-23
 ; PRIOR APPLICATION NUMBER: US 10/226615
 ; PRIOR FILING DATE: 2002-08-23
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-374-932-5
 Query Match 100.0% ; Score 33; DB 4; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TYWIG 5
 Db 1 TYWIG 5

RESULT 2
 US-10-379-741-5
 ; Sequence 5, Application US/10379741
 ; Publication No. US20040071702A1
 ; GENERAL INFORMATION:
 ; APPLICANT: van de Winkel, Jan G.J.
 ; APPLICANT: van Dijk, Marcus Antonius
 ; APPLICANT: Schuurman, Janine
 ; APPLICANT: Gerritsen, Arnout F.
 ; APPLICANT: Baadsgaard, Ole
 ; APPLICANT: Petersen, Jorgen
 ; TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)
 ; FILE REFERENCE: GMI -024CP2
 ; CURRENT APPLICATION NUMBER: US/10/379,741

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; CURRENT FILING DATE: 2003-03-05 ; NUMBER OF SEQ ID NOS: 138
; PRIOR FILING DATE: 2001-08-23 ; SOFTWARE: PatentIn version 3.0
; PRIOR APPLICATION NUMBER: US ; SEQ ID NO: 92
; LENGTH: 5
; TYPE: PRT
; ORGANISM: homo sapien
US-10-891-658-92

RESULT 5
Query Match 100.0%; Score 33; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 1 TYWIG 5

RESULT 5
US-10-982-725-5
Query Match 100.0%; Score 33; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 1 TYWIG 5

RESULT 3
US-10-769-144-13
Sequence 13, Application US/10769144
; PUBLIC INFORMATION: US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; ENDRES, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFORE
; FILE REFERENCE: MXI-301
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 13
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-13

Query Match 100.0%; Score 33; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 1 TYWIG 5

RESULT 6
US-10-903-191-13
Sequence 13, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: He, Lizhen
; APPLICANT: Keler, Tibor
; ENDRES, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFORE
; FILE REFERENCE: MXI-301CP
; CURRENT FILING DATE: 2004-07-0
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 13
; LENGTH: 5
; TYPE: PRT

RESULT 4
US-10-891-658-92
Sequence 92, Application US/10891658
; PUBLIC INFORMATION: US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 02-1240
; CURRENT FILING NUMBER: US/10/891,658
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,431
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 13
; LENGTH: 5
; TYPE: PRT

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; ORGANISM: Homo sapiens
 us-10-903-191-13

Query Match 100.0%; Score 33; DB 5; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
 Db 1 TYWIG 5

RESULT 7
 US-10-437-963-106931
 ; Sequence 106931, Application US/10437963
 ; Publication No. US20040123334A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovacic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO: 106931
 ; LENGTH: 76

; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT4530_11330C.1.pep
 us-10-437-963-106931

Query Match 100.0%; Score 33; DB 4; Length 76;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
 Db 9 TYWIG 13

RESULT 8
 US-10-803-622-172
 ; Sequence 172, Application US/10803622
 ; Publication No. US20040157214A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cambridge Antibody Technology Limited
 ; APPLICANT: Cambridge Antibody Technology Limited
 ; APPLICANT: Medical Research Council
 ; APPLICANT: McCafferty, John
 ; APPLICANT: Pope, Anthony
 ; APPLICANT: Johnson, Kevin
 ; APPLICANT: Hoogenboom, Hendricus
 ; APPLICANT: Griffiths, Andrew
 ; APPLICANT: Jackson, Ronald
 ; APPLICANT: Holliger, Kasper
 ; APPLICANT: Clackson, Timothy
 ; APPLICANT: Marks, James
 ; APPLICANT: Chiwell, David
 ; APPLICANT: Winter, Gregory
 ; APPLICANT: Bonert, Timothy
 ; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
 ; FILE REFERENCE: 13839-00013
 ; CURRENT APPLICATION NUMBER: US/10/803,653
 ; CURRENT FILING DATE: 2004-03-18
 ; PRIOR APPLICATION NUMBER: GB 9015198.6
 ; PRIOR FILING DATE: 1990-07-10
 ; PRIOR APPLICATION NUMBER: GB 9022845.3
 ; PRIOR FILING DATE: 1990-10-19
 ; PRIOR APPLICATION NUMBER: GB 9024503.6
 ; PRIOR FILING DATE: 1990-11-12
 ; PRIOR APPLICATION NUMBER: GB 9104744.9
 ; PRIOR FILING DATE: 1991-03-06
 ; PRIOR APPLICATION NUMBER: GB 9110549.4
 ; PRIOR FILING DATE: 1991-05-15
 ; PRIOR APPLICATION NUMBER: PCT/GB91/01134
 ; PRIOR FILING DATE: 1991-07-10
 ; PRIOR APPLICATION NUMBER: US 07/971,857
 ; PRIOR FILING DATE: 1993-01-08
 ; PRIOR APPLICATION NUMBER: US 08/484,893
 ; NUMBER OF SEQ ID NOS: 272
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 172
 ; LENGTH: 88

; TYPE: PRT
 ; ORGANISM: Homo sapiens
 us-10-803-622-172

RESULT 9
 US-10-803-653-172
 ; Sequence 172, Application US/10803653
 ; Publication No. US20040157215A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cambridge Antibody Technology Limited
 ; APPLICANT: Cambridge Antibody Technology Limited
 ; APPLICANT: Medical Research Council
 ; APPLICANT: McCafferty, John
 ; APPLICANT: Pope, Anthony
 ; APPLICANT: Johnson, Kevin
 ; APPLICANT: Hoogenboom, Hendricus
 ; APPLICANT: Griffiths, Andrew
 ; APPLICANT: Jackson, Ronald
 ; APPLICANT: Holliger, Kasper
 ; APPLICANT: Clackson, Timothy
 ; APPLICANT: Marks, James
 ; APPLICANT: Chiwell, David
 ; APPLICANT: Winter, Gregory
 ; APPLICANT: Bonert, Timothy
 ; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
 ; FILE REFERENCE: 13839-00013
 ; CURRENT APPLICATION NUMBER: US/10/803,653
 ; CURRENT FILING DATE: 2004-03-18
 ; PRIOR APPLICATION NUMBER: GB 9015198.6
 ; PRIOR FILING DATE: 1990-07-10
 ; PRIOR APPLICATION NUMBER: GB 9022845.3
 ; PRIOR FILING DATE: 1990-10-19
 ; PRIOR APPLICATION NUMBER: GB 9024503.6
 ; PRIOR FILING DATE: 1990-11-12
 ; PRIOR APPLICATION NUMBER: GB 9104744.9
 ; PRIOR FILING DATE: 1991-03-06
 ; PRIOR APPLICATION NUMBER: GB 9110549.4
 ; PRIOR FILING DATE: 1991-05-15
 ; PRIOR APPLICATION NUMBER: PCT/GB91/01134
 ; PRIOR FILING DATE: 1991-07-10
 ; PRIOR APPLICATION NUMBER: US 07/971,857

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; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-035-637-4

Query Match 100.0%; Score 33; DB 4; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

RESULT 12
US-10-769-144-4
Sequence 4, Application US/10769144
Publication No. US20040248215A1
GENERAL INFORMATION:
APPLICANT: Keler, Tibor
APPLICANT: Endres, Michael
APPLICANT: He, Lizhen
APPLICANT: Ramakrishna, Venky
TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
FILE REFERENCE: MXI-301
CURRENT APPLICATION NUMBER: US/10/769,144
CURRENT FILING DATE: 2004-01-30
PRIOR APPLICATION NUMBER: 60/443979
PRIOR FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4

RESULT 13
US-10-903-191-4
Sequence 4, Application US/10903191
Publication No. US20050180583A1
GENERAL INFORMATION:
APPLICANT: Keler, Tibor
APPLICANT: Endres, Michael
APPLICANT: He, Lizhen
APPLICANT: Ramakrishna, Venky
TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
FILE REFERENCE: MXI-301
CURRENT APPLICATION NUMBER: US/10/903,191
CURRENT FILING DATE: 2004-07-30
PRIOR APPLICATION NUMBER: 10/769144
PRIOR FILING DATE: 2004-01-30
PRIOR APPLICATION NUMBER: 60/443979
PRIOR FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 116

RESULT 14
US-10-851-614-4
Sequence 4, Application US/09851614
Publication No. US20030167502A1
GENERAL INFORMATION:
APPLICANT: Keler, Tibor
APPLICANT: Deo, Yashwant M.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC CELLS
FILE REFERENCE: MXI-166
CURRENT APPLICATION NUMBER: US/09/851,614
CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: US/09/851,614
PRIOR FILING DATE: 2000-05-08
PRIOR APPLICATION NUMBER: USSN 60/230,739
PRIOR FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 116
TYPE: PRT
ORGANISM: Homo sapiens
US-10-851-614-4

RESULT 15
US-10-903-191-4
Sequence 4, Application US/10903191
Publication No. US20050180583A1
GENERAL INFORMATION:
APPLICANT: Keler, Tibor
APPLICANT: Endres, Michael
APPLICANT: He, Lizhen
APPLICANT: Ramakrishna, Venky
TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
FILE REFERENCE: MXI-301
CURRENT APPLICATION NUMBER: US/10/903,191
CURRENT FILING DATE: 2004-07-30
PRIOR APPLICATION NUMBER: 10/769144
PRIOR FILING DATE: 2004-01-30
PRIOR APPLICATION NUMBER: 60/443979
PRIOR FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 116

RESULT 16
US-10-035-637-4
Sequence 4, Application US/10035637
Publication No. US2003031667A1
GENERAL INFORMATION:
APPLICANT: Keler, Tibor
APPLICANT: Deo, Yashwant M.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC CELLS
FILE REFERENCE: MXI-166CP
CURRENT APPLICATION NUMBER: US/10/035,637
CURRENT FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 09/851,614
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USSN 60/203,126
PRIOR FILING DATE: 2000-05-08
PRIOR APPLICATION NUMBER: USSN 60/230,739
PRIOR FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 116
TYPE: PRT
ORGANISM: Homo sapiens
US-10-903-191-4

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Query	Match Best Local Matches	Similarity Score 33; Pred. No. 0;	DB 5; Length 116; Mismatches 0;	Indels 0;	Gaps 0;	Qy 1 TYWIG 5 Db 31 TYWIG 35	1 TYWIG 5 31 TYWIG 35
RESULT 14	US-10-891-658-79						
	; Sequence 79, Application US/10891658						
	; Publication No. US20050074821A1						
	; GENERAL INFORMATION:						
	; APPLICANT: Kenneth, Wild						
	; APPLICANT: Treanor, James						
	; APPLICANT: Huang, Haichun						
	; APPLICANT: Inoue, Heather						
	; APPLICANT: Zhang, Tie J.						
	; APPLICANT: Martin, Frank						
	; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway						
	; TITLE OF INVENTION: Inhibitors						
	; FILE REFERENCE: 02-1240						
	; CURRENT APPLICATION NUMBER: US/10/891,658						
	; CURRENT FILING DATE: 2004-07-15						
	; PRIOR APPLICATION NUMBER: US 60/487,431						
	; PRIOR FILING DATE: 2003-07-15						
	; NUMBER OF SEQ ID NOS: 138						
	; SOFTWARE: PatentIn version 3.0						
	; SEQ ID NO 79						
	; LENGTH: 125						
	; TYPE: PRT						
	; ORGANISM: homo sapien						
	US-10-891-658-79						
RESULT 15	US-10-226-615-2						
	; Sequence 2, Application US/10226615						
	; Publication No. US20030138421A1						
	; GENERAL INFORMATION:						
	; APPLICANT: van de Winkel, Jan G.J.						
	; APPLICANT: van Dijk, Marcus Antonius						
	; APPLICANT: Gerritsen, Arnout F.						
	; APPLICANT: Schuurman, Janine						
	; APPLICANT: Baadsgaard, Ole						
	; TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)						
	; FILE REFERENCE: GMT-024						
	; CURRENT APPLICATION NUMBER: US/10/226,615						
	; CURRENT FILING DATE: 2002-08-23						
	; PRIOR APPLICATION NUMBER: US 60/314,731						
	; PRIOR FILING DATE: 2001-08-23						
	; NUMBER OF SEQ ID NOS: 4						
	; SOFTWARE: FastSEQ for Windows Version 4.0						
	; SEQ ID NO 2						
	; LENGTH: 130						
	; TYPE: PRT						
	; ORGANISM: Homo sapiens						
	US-10-226-615-2						

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Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	248	7 US-11-054-515-1	Sequence 1, Appli
2	29	87.9	98	7 US-11-054-554-45	Sequence 45, Appli
3	29	87.9	98	7 US-11-054-554-56	Sequence 56, Appli
4	29	87.9	252	7 US-11-054-515-1537	Sequence 1537, Appli
5	28	84.8	157	6 US-10-467-626-1168	Sequence 1168, Appli
6	28	84.8	163	6 US-10-467-657-6140	Sequence 6140, Appli
7	28	84.8	249	7 US-11-054-515-1312	Sequence 1312, Appli
8	28	84.8	254	7 US-11-054-515-873	Sequence 873, Appli
9	28	84.8	254	7 US-11-054-515-888	Sequence 888, Appli
10	28	84.8	254	7 US-11-054-515-1087	Sequence 1087, Appli
11	28	84.8	254	7 US-11-054-515-1088	Sequence 1088, Appli
12	28	84.8	372	6 US-10-844-035-1	Sequence 1, Appli
13	28	84.8	582	7 US-11-074-176-110	Sequence 110, Appli
14	27	81.8	117	6 US-10-821-234-1253	Sequence 1253, Appli
15	27	81.8	314	7 US-11-104-172-1110	Sequence 1110, Appli
16	27	81.8	372	6 US-10-131-826-106	Sequence 106, Appli
17	27	81.8	416	6 US-10-821-234-1175	Sequence 1375, Appli
18	26	78.8	118	6 US-10-793-626-2630	Sequence 2630, Appli
19	26	78.8	130	6 US-10-467-657-3470	Sequence 3470, Appli
20	26	78.8	163	6 US-10-467-657-852	Sequence 852, Appli
21	26	78.8	178	6 US-10-467-657-2108	Sequence 2108, Appli
22	26	78.8	232	6 US-10-793-626-1602	Sequence 1602, Appli
23	26	78.8	244	6 US-10-821-234-1264	Sequence 1264, Appli
24	26	78.8	253	7 US-11-054-515-1003	Sequence 1003, Appli
25	26	78.8	253	7 US-11-054-515-1007	Sequence 1007, Appli

US-11-054-669-45
 / Sequence 45; Application US/11054669
 / Publication No. US2005026180A1
 / GENERAL INFORMATION:
 / APPLICANT: Foote, Jefferson
 / TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
 / FILE REFERENCE: 30219/US/3
 / CURRENT APPLICATION NUMBER: US/11/054, 669
 / CURRENT FILING DATE: 2005-02-08
 / PRIORITY FILING DATE: US/10/194, 975
 / PRIOR APPLICATION NUMBER: US/60/305, 111
 / PRIOR FILING DATE: 2001-07-12
 / NUMBER OF SEQ ID NOS: 124
 / SOFTWARE: PatentIn Version 3.3
 / SEQ ID NO 45
 / LENGTH: 98
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-11-054-669-45

Query Match Similarity 87.9%; Score 29; DB 7; Length 98;
 Best Local Similarity 80.0%; Pred. No. 15; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 0;

Qy 1 TYWIG 5
 Db 31 SYWIG 35

RESULT 3
 US-11-084-554-56
 / Sequence 56; Application US/11084554
 / Publication No. US20050260679A1
 / GENERAL INFORMATION:
 / APPLICANT: Kellermann, Sirid-Ai
 / APPLICANT: Green, Larry L.
 / APPLICANT: Korver, Wouter
 / TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
 / TITLE OF INVENTION: ANTIODIES THROUGH V GENE MANIPULATION
 / FILE REFERENCE: ABEQUINX-100A
 / CURRENT APPLICATION NUMBER: US/11084, 554
 / CURRENT FILING DATE: 2005-03-17
 / PRIOR APPLICATION NUMBER: 60/554, 372
 / PRIOR FILING DATE: 2004-03-19
 / PRIOR APPLICATION NUMBER: 60/574, 661
 / PRIOR FILING DATE: 2004-05-24
 / NUMBER OF SEQ ID NOS: 266
 / SOFTWARE: PatentSEQ for Windows Version 4.0
 / SEQ ID NO 56
 / LENGTH: 98
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-11-084-554-56

Query Match Similarity 87.9%; Score 29; DB 7; Length 98;
 Best Local Similarity 80.0%; Pred. No. 15; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 0;

Qy 1 TYWIG 5
 Db 31 SYWIG 35

RESULT 4
 US-11-054-515-1537
 / Sequence 1537; Application US/11054515
 / Publication No. US2005025552A1
 / GENERAL INFORMATION:
 / APPLICANT: Ruben et al.
 / TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 / FILE REFERENCE: PF523P3
 / CURRENT APPLICATION NUMBER: US/11054, 515

Query Match Similarity 87.9%; Score 29; DB 7; Length 98;
 Best Local Similarity 80.0%; Pred. No. 15; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 0;

Qy 1 TYWIG 5
 Db 31 SYWIG 35

RESULT 5
 US-10-793-626-1168
 / Sequence 1168; Application US/10793626
 / Publication No. US20050255478A1
 / GENERAL INFORMATION:
 / APPLICANT: KIMMELLY, WILLIAM JOHN
 / TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 / FILE REFERENCE: PU3480US
 / CURRENT FILING DATE: 2004-03-04
 / PRIOR APPLICATION NUMBER: 60/164, 258
 / PRIOR FILING DATE: 1999-11-09
 / NUMBER OF SEQ ID NOS: 4472
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 1168
 / LENGTH: 157
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: synthetic
 / OTHER INFORMATION: amino acid sequence
 US-10-793-626-1168

Query Match Similarity 87.9%; Score 29; DB 7; Length 98;
 Best Local Similarity 80.0%; Pred. No. 32; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;

Qy 2 YWIG 5
 Db 112 YWIG 115

RESULT 6
 US-10-467-657-6140
 / Sequence 6140; Application US/10467657

Publication No. US20050260581A1
 GENERAL INFORMATION:
 APPLICANT: CHIRON SPA
 APPLICANT: PIZZA, Mariagrazia
 APPLICANT: MASNIGNANI, Vega
 APPLICANT: MONACI, Elisabetta
 TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 FILE REFERENCE:
 CURRENT APPLICATION NUMBER: US 10/467,657
 CURRENT FILING DATE: 2003-08-11
 PRIOR APPLICATION NUMBER: GB-0103424.8
 PRIOR FILING DATE: 2001-02-12
 NUMBER OF SEQ ID NOS: 9218
 SOFTWARE: SeqWin9, version 1.04
 SEQ ID NO: 6140
 LENGTH: 163
 TYPE: PRT
 ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-6140

Query Match 84.8%; Score 28; DB 6; Length 163;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWIG 5
 Db 113 YWIG 116

RESULT 7
 US-11-054-515-1312
 Sequence 1312, Application US/11054515
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 FILE REFERENCE: PP523P3
 CURRENT APPLICATION NUMBER: US/11/054,515
 CURRENT FILING DATE: 2005-02-10
 PRIOR APPLICATION NUMBER: 60/543,296--
 PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: 60/580,347
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 10/293,418
 PRIOR FILING DATE: 2002-11-14
 PRIOR APPLICATION NUMBER: 60/331,469
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/340,817
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-05

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 3247

SEQ ID NO: 1312
 LENGTH: 249
 TYPE: PRT
 ORGANISM: Homo sapiens

US-11-054-515-1312
 Query Match 84.8%; Score 28; DB 7; Length 249;

Best Local Similarity 100.0%; Pred. No. 47;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWIG 5

Db 32 YWIG 35

RESULT 8
 US-11-054-515-873
 Sequence 873, Application US/11054515
 Publication No. US20050255532A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 FILE REFERENCE: PP523P3
 CURRENT APPLICATION NUMBER: US/11/054,515
 CURRENT FILING DATE: 2005-02-10
 PRIOR APPLICATION NUMBER: 60/543,296
 PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: 60/580,347
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 10/293,418
 PRIOR FILING DATE: 2002-11-14
 PRIOR APPLICATION NUMBER: 60/331,469
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/340,817
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 09/880,748
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: 60/331,469
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/340,817
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 09/880,748
 PRIOR FILING DATE: 2001-06-15

Query Match 84.8%; Score 28; DB 7; Length 254;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWIG 5
 Db 32 YWIG 35

RESULT 9
 US-11-054-515-888
 Sequence 888, Application US/11054515
 Publication No. US20050255532A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 FILE REFERENCE: PP523P3
 CURRENT APPLICATION NUMBER: US/11/054,515
 CURRENT FILING DATE: 2005-02-10
 PRIOR APPLICATION NUMBER: 60/543,296
 PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: 60/580,347
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 10/293,418
 PRIOR FILING DATE: 2002-11-14
 PRIOR APPLICATION NUMBER: 60/331,469
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/340,817
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 09/880,748
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: 60/331,469
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/340,817
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 09/880,748
 PRIOR FILING DATE: 2001-06-15

Query Match 84.8%; Score 28; DB 7; Length 254;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWIG 5

PRIOR APPLICATION NUMBER: 60/293,499
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/277,379
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/276,248
 PRIOR FILING DATE: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/240,816
 PRIOR FILING DATE: 2000-10-17
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 3247
 SEQ ID NO: 888
 LENGTH: 254
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-054-515-888

Query Match 84.8%; Score 28; DB 7; Length 254;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWIG 5
 Db 32 YWIG 35

RESULT 10
 US-11-054-515-1087
 Sequence 1087, Application US/11054515
 Publication No. US20050255532A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 FILE REFERENCE: PF523P3
 CURRENT APPLICATION NUMBER: US/11/054,515
 CURRENT FILING DATE: 2005-02-10
 PRIOR APPLICATION NUMBER: 60/543,296
 PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: 60/580,347
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 10/293,418
 PRIOR FILING DATE: 2002-11-14
 PRIOR APPLICATION NUMBER: 60/331,469
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/340,817
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 09/980,748
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: 60/293,499
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/277,379
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 3247
 SEQ ID NO: 1088
 LENGTH: 254
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-054-515-1088

Query Match 84.8%; Score 28; DB 7; Length 254;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWIG 5
 Db 32 YWIG 35

RESULT 12
 US-10-844-035-1
 Sequence 1, Application US/10844035
 Publication No. US20050255598A1
 GENERAL INFORMATION:
 APPLICANT: ROSEN, STEVEN D.
 APPLICANT: NOBLE, LINDA J.
 TITLE OF INVENTION: METHODS OF TREATING TRAUMATIC SPINAL
 INJURY
 TITLE OF INVENTION: CORD INJURY
 FILE REFERENCE: UCAL-319
 CURRENT APPLICATION NUMBER: US/10/844,035
 CURRENT FILING DATE: 2004-05-11
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 1
 LENGTH: 372
 TYPE: PRT
 ORGANISM: homo sapien
 US-10-844-035-1

Query Match 84.8%; Score 28; DB 6; Length 372;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWIG 5
 Db 87 YWIG 90

RESULT 11

RESULT 13
US-11-074-176-110
Sequence 110, Application US/11074176
Publication No. US20050250135A1
GENERAL INFORMATION:
APPLICANT: Klaenhammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: Alterman, Eric
APPLICANT: McAuliffe, Olivia
APPLICANT: Peril, Andrea Azcarate
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Stress-Related Proteins and Uses Thereof
TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
FILE REFERENCE: 5051-94
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 110
LENGTH: 582
TYPE: PRT
ORGANISM: Lactobacillus acidophilus
US-11-074-176-110

Query Match Score 84.8%; DB 7; Length 582;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;

Qy 2 YWIG 5
Db 128 YWIG 131

RESULT 14
US-10-821-234-1253
Sequence 1253, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: B1A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
NUMBER OF SEQ ID NOS: 1704
SEQ ID NO 1253
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-1253

Query Match Score 81.8%; DB 6; Length 117;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 3; Conservative 1; Mismatches 0; Gaps 0;
Indels 0;

Qy 2 YWIG 5
Db 68 YWIG 71

RESULT 15
US-11-108-172-1110
Sequence 1110, Application US/11108172
Publication No. US20050260177A1
GENERAL INFORMATION:

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Scoring table:	BLOSUM62	
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Searched:	2443163 seqs,	439378781 residues
Total number of hits satisfying chosen parameters:	2443163	
Title:	US-10-769-144-14	
Perfect score:	92	
Sequence:	1 IYPGDSDTIYSPSFQG 17	
OM protein - protein search, using SW model		
Run on:	December 3, 2005, 14:10:00 ; Search time 29:07:35 Seconds (without alignments) 256.916 Million cell updates/sec	
Aea18876	Amino acid	AEA18876
Copyright (c) 1993 - 2005 Compugen Ltd.		
Aaw62197	Amino acid	AAW62197
Aaw54008	Human Ant	AAW54008
Abg78333	Human Fv	ABG78333
Abg78331	Human Fv	ABG78331
Abg78322	Human Fv	ABG78322
Abg91924	Human ant	ABG91924
Abg91922	Human ant	ABG91922
Abg91923	Human ant	ABG91923
Abu56809	Human Imm	ABU56809
Abp56508	Human ant	ABP56508
Abj18867	Antibody	ABJ18867
Abo27112	Human ger	ABO27112
Add69247	Human hea	ADD69247
Adf10156	Antibody	ADF10156
Adf09948	Antibody	ADF09948
Adf10053	VEGF anti	ADF10053
Adk18943	Anti-huma	ADK18943
Adk18888	Anti-huma	ADK18888
Adk18877	Anti-huma	ADK18877
Adk18878	Anti-huma	ADK18878

ALIGNMENTS

RESULT 1

6831 ADR46831 standard; peptide; 17 AA.
ADR46831;
18-NOV-2004 (first entry)
Human antibody B11 heavy chain variable region CDR2 SEQ ID NO:14.
molecular conjugate; monoclonal antibody; human antigen presenting cell; antigen presenting cell; APC; human; beta human chorionic gonadotropin; betahCG; beta chorionic gonadotropin; antibody; T cell-mediated immune response; immunoprotection; cytosolic; antimicrobial; immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial; CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease; melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes; antibody B11; heavy chain variable region; CDR; complementarity determining region.

Homo sapiens.
WO2004074432-A2.
02-SEP-2004.

30-JAN-2004; 2004W0-US002725.

31-JAN-2003; 2003US-0443979P.

(MEDA-) MEDAREX INC.

Keler T, Endres M, He L, Ramakrishna V;
WPI; 2004-635555/61.

Claim 8; SEQ ID NO 14; 82pp; English.

New molecular conjugate having a monoclonal antibody that binds to human APCs linked to a beta human chorionic gonadotropin, useful for inducing a cytotoxic T cell response in cancers and infectious diseases.

The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (APCs) linked to beta human chorionic gonadotropin (betahCG), where the antibody comprises a heavy and/or light chain variable region derived from a human vHc5.51 or vLc115 derivative sequence with the 98 or 95 amino acid sequences

MANAGEMENT

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : A_Geneseq_21:
 1:_geneseq1900s:
 ID ADR16831 standard; peptide; 1 / AA;
 XX
 AC ADR16831;

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3: geneseqP2000s;*
4: geneseqP2001s;*
5: geneseqP2002s;*
6: geneseqP2003s;*
7: geneseqP2003b;*
8: geneseqP2004s;*
9: geneseqP2005s;*
XX 18-NOV-2004 (first entry)
DT XX
DB XX
KW XX
KW XX
KW XX
KW XX
KW XX
KW XX

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the distribution and is derived by analysis of the total score distribution.

MAPTEC

CC of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
 CC described; (1) a molecular conjugate comprising a human antibody heavy
 CC chain and a human antibody light chain, where either or both chains are
 CC linked to betahCG; (2) a molecular conjugate comprising a human single
 CC chain antibody that binds to human APCs linked to betahCG, where the
 CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
 CC (ADR46829); (3) a composition comprising any of the molecular conjugates
 CC as described above, and a carrier, optionally in combination with an
 CC adjuvant; (4) inducing or enhancing T cell-mediated immune response,
 CC against betahCG, comprising contacting any of the molecular conjugates
 CC described above with APCs such that the antigen is processed and
 CC presented to T cells in a manner which induces or enhances T cell-
 CC mediated response against the antigen; (5) immunising a subject
 CC comprising administering any of the molecular conjugates described above,
 CC optionally in combination with an adjuvant, cytokine which stimulates
 CC proliferation of dendritic cells and/or an immunostimulatory agent; and
 CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,
 CC comprising forming a conjugate of the antigen and monoclonal antibody
 CC which binds to APCs, and contacting the conjugate either in vivo or ex
 CC vivo with APCs such that the antigen is internalised, processed and
 CC presented to T cells in a manner which induces or enhances a cytotoxic T
 CC cell response against the antigen. The molecular conjugate has
 CC cytotoxic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
 CC virucide and antimarial activities, and can be used as a CD8 agonist,
 CC and in vaccines. The methods and compositions of the present invention
 CC are useful for inducing a cytotoxic T cell response, and in particular
 CC for treating autoimmune disorders, cancer and infectious diseases by
 CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
 CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
 CC herpes. The present sequence represents the human antibody B11 heavy
 CC chain variable region complementary determining region 2 (CDR2) amino
 CC acid sequence, which is used in the exemplification of the present
 CC invention.

XX Sequence 17 AA;
 SQ Query Match Score 92; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 IIFYPGDSDTIYSPSQG 17
 Db 1 IIFYPGDSDTIYSPSQG 17
 1 IIFYPGDSDTIYSPSQG 17

RESULT 2
 AAM46005 Standard; protein; 116 AA.
 XX AC AAM46005;
 XX DT 08-MAR-2002 (first entry)

DE Human monoclonal antibody B11 variable heavy chain protein.
 XX Human; monoclonal antibody; B11; antigen binding portion; dendritic cell;
 KW mannose receptor; growth; cytolysis; pathogen; virus; bacterium;
 KW autoimmune disease; inflammatory disorder; rheumatoid arthritis;
 KW multiple sclerosis; diabetes mellitus; immunomodulatory;
 KW antiinflammatory; antirheumatic; antiarthritic; neuroprotective;
 KW antidiabetic; antianæmic; endocrine; dermatological; antithyroid;
 KW uropathic; ophthalmological; muscular.
 XX Homo sapiens.

OS XX WO200185798-A2.
 PN XX PD 15-NOV-2001.
 XX PR 08-MAY-2001; 2001WO-US015114.
 PR 08-MAY-2000; 2000US-0203126P.
 PR 07-SEP-2000; 2000US-0230739P.

XX (MEDA-) MEDAREX INC.
 PA Deo YM, Keler T;
 PI XX DR WPI; 2002-089788/12.
 N-PSDB; ABA05100.

XX Example 2; Fig 13; 95pp; English.

XX The invention relates to human monoclonal antibodies or their antigen
 CC binding portions that specifically bind to dendritic cells and has one or
 CC more of the following characteristics: (a) binding affinity constant to a dendritic cell of at least about 10 to the power 7 M-1; (b) the ability
 CC to opsonise a dendritic cell; (c) the ability to internalise after
 CC binding to a dendritic cell; or (d) the ability to activate dendritic
 CC cells. The isolated human monoclonal antibody or its antigen binding
 CC portion may also have any of the following characteristics: (a) mediates
 CC cytolysis of dendritic cells in the presence of human effector cells; or
 CC (b) inhibits growth of dendritic cells. The antibodies or its antigen
 CC binding portion, binds to and blocks the human mannose receptor on
 CC dendritic cells. The antibodies have immunomodulatory, antinflammatory,
 CC antirheumatic, antilarthritic, neuroprotective, antidiabetic, antianæmic,
 CC endocrine, dermatological, antithyroid, uropathic, ophthalmological and
 CC muscular activity. The antibodies or their antigen-binding fragments are
 CC useful for inhibiting growth of a dendritic cell, inducing cytolysis of a
 CC dendritic cell, treating or preventing a dendritic cell mediated disease,
 CC detecting the presence of a dendritic cell, targeting an antigen to a
 CC dendritic cell and preventing binding of a pathogen (a virus or a
 CC bacterium) to human mannose receptor on dendritic cells. In particular,
 CC the antibodies may be used to treat, autoimmune disease, graft versus
 CC host disease, immune system or inflammatory disorders (e.g. rheumatoid
 CC arthritis), multiple sclerosis, diabetes mellitus, myasthenia gravis,
 CC pernicious anaemia, Addison's disease, lupus erythematosus, Reiter's
 CC syndrome and Graves disease. The present sequence is that of the human
 CC monoclonal antibody B11 variable heavy chain, useful to the invention

XX SQ Sequence 116 AA;
 SQ Query Match Score 92; DB 5; Length 116;
 Best Local Similarity 100.0%; Pred. No. 4.3e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIFYPGDSDTIYSPSQG 17
 Db 50 IIFYPGDSDTIYSPSQG 66
 SQ Sequence 116 AA;

RESULT 3
 ADR46821 standard; protein; 116 AA.
 XX AC ADR46821;
 XX DT 18-NOV-2004 (first entry)

XX Human antibody B11 heavy chain variable region protein SEQ ID NO:4.
 KW molecular conjugate; monoclonal antibody; human antigen presenting cell;
 KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
 KW betahCG; beta chorionic gonadotropin; antibody;
 KW T cell-mediated immune response; immunisation; cytostatic; antimalarial;
 KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
 KW CDB agonist; vaccine; autoimmune disorder; cancer; infectious disease;
 KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
 KW antibody B11; heavy chain variable region.
 OS Homo sapiens.

ID	ADR46829	standard; protein; 411 AA.		
XX	PN	WO2004074432-A2.		
XX	PD	02-SEP-2004.		
XX	PR	30-JAN-2004; 2004WO-US002725.		
XX	PR	31-JAN-2003; 2003US-0443979P.		
PA	(MEDA -) MEDAREX INC.			
PTI	Keler T,	Endres M,	He L,	Ramakrishna V;
XX	WPI:	2004-635555/61.		
DR	N-PSDB;	ADR46829.		
XX	New molecular conjugate having a monoclonal antibody that binds to human APCs linked to a beta human chorionic gonadotropin, useful for inducing a cytotoxic T-cell response in cancers and infectious diseases.			
XX	Claim 11; SEQ ID NO 4; 82pp; English.			
CC	The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (APCs) linked to beta human chorionic gonadotropin (betahCG), where the antibody comprises a heavy and/or light chain variable region derived from a human VH5-51 or VK-L15 germline sequence with the 98 or 95 amino acid sequences of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are linked to betahCG; (2) a molecular conjugate comprising a human single chain antibody that binds to human APCs linked to betahCG, where the conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an adjuvant; (4) inducing or enhancing a T cell mediated immune response, against betahCG, comprising contacting any of the molecular conjugates described above with APCs such that the antigen is processed and presented to T cells in a manner which induces or enhances a T cell-mediated response against the antigen; (5) immunising a subject comprising administering any of the molecular conjugates described above, optionally in combination with an adjuvant, cytokine which stimulates proliferation of dendritic cells and/or an immunostimulatory agent; and (6) inducing or enhancing a cytotoxic T cell response against an antigen, comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either <i>in vivo</i> or <i>ex vivo</i> with APCs such that the antigen is internalised, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate has cyrostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic, virucide and antimalarial activities, and can be used as a CD8 agonist, and in vaccines. The methods and compositions of the present invention are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukemia, HIV, hepatitis, malaria and herpes. The present sequence represents a human antibody B11 heavy chain variable region, which is used in the exemplification of the present invention.			
XX	Sequence 116 AA;			
SQ	Score 92; DB 8; Length 116;			
Query Match 1	100.0%	Pred. No. 4.3e-06;		
Best Local Similarity	100.0%	Mismatches 0;		
Matches 17;	Conservative 0;	Indels 0;		
Gaps	0;	0;		
Qy	1 I I Y P G D S D T I Y S P S P S Q C	17		
Db	50 I I Y P G D S D T I Y S P S P S Q C	66		
RESULT 4				
ADR46829				

described above with APCs such that the antigen is processed and presented to T cells in a manner which induces or enhances a T cell-mediated response against the antigen; (5) immunising a subject comprising administering any of the molecular conjugates described above, optionally in combination with an adjuvant, a cytokine which stimulates proliferation of dendritic cells and/or an immunomodulatory agent; and (6) inducing or enhancing a cytotoxic T cell response against an antigen, comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either *in vivo* or *ex vivo* with APCs such that the antigen is internalised, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate has cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic, virucide and antimalarial activities and can be used as a CD8 agonist, and in vaccines. The methods and compositions of the present invention are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents a human antibody B11 heavy chain variable region, which is used in the exemplification of the present invention.

US Homo sapiens.

XX WO2004074432-A2.

PN XX

XX PD 02-BEP-2004.

XX P 30-JAN-2004; 2004WO-US002725.

PP XX

PR 31-JAN-2003; 2003US-0443979P.

XX PA (MEDA-) MEDAREX INC.

XX PI Kehler T, Endres M, He L, Ramakrishna V;

XX DR WPI; 2004-6335555/61.

DR N-PSDB; ADR46818.

XX PT New molecular conjugate having a monoclonal antibody that binds to human chorionic gonadotropin (berahCG), where the antibody APCs linked to a beta human chorionic gonadotropin, useful for inducing a cytotoxic T cell response in cancers and infectious diseases.

PT XX

PT Claim 13; SEQ ID NO 2; 82pp; English.

PS XX

CC The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (APCs) linked to beta human chorionic gonadotropin (berahCG), where the antibody comprises a heavy and/or light chain variable region derived from a human VH5-51 or VK-L15 germline sequence with the 98 or 95 amino acid sequences of SEQ ID NO:30 or 32 (ADR46847, or ADR46819), respectively. Also described, (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are linked to berahCG, (2) a molecular conjugate comprising a human single chain antibody that binds to human APCs linked to berahCG, where the conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an adjuvant, (4) inducing or enhancing T cell mediated immune response, against berahCG, comprising contacting any of the molecular conjugates

cytotoxic T cell response in cancers and infectious diseases.

Example 1; SEQ ID NO 10; 82pp; English.

XX PN WO2004056874-A2.
 PS XX 08-JUL-2004.
 XX PD 22-DEC-2003; 2003WO-EP014756.
 CC XX 20-DEC-2002; 2002US-0435893P.
 CC PR 15-JAN-2003; 2003EP-0000615.
 CC PA (XERI-1) XERION PHARM AG.
 CC PA (TUFTS) UNIV TUFTS.
 CC XX
 CC Unger CM, Beste G, Zehetmeier C, Lain B, Torella C, Nieuweltner J;
 CC PI Jay DG, Bustace BK, Krauer R, Jensen KH;
 CC XX
 CC DR WPI: 2004-507700/48.
 CC DR N-PSDB; ADR28100.
 CC XX
 CC PT Novel neuropilin binder which is scFv, antibody fragment or bioconjugate,
 CC PT that modulates neuropilin-1 function or inhibits NP-1 dependent
 CC PT angiogenesis of endothelial cells and/or invasion of tumor cells useful
 CC PT for treating cancer.
 CC XX
 CC PS Claim 3; SEQ ID NO 13; 120pp; English.
 CC XX
 CC The invention relates to a neuropilin binder (NPB) (I) which is a
 CC polypeptide, antibody, scfv, antibody fragment or bioconjugate, that
 CC modulates neuropilin-1 (NP-1) function or inhibits NP-1 dependent
 CC angiogenesis of endothelial cells and/or invasion of tumour cells,
 CC whereby the NPB binds to NP-1 and modulates NP-1 function. Further
 CC disclosed is an ex vivo method of determining the dependency of the
 CC invasiveness of naturally occurring invasive cancer cell on the
 CC functionality of NP-1. The NPB of the invention is an inhibitor of
 CC metastasis of NP-1 mediated invasion and/or adhesion and an inhibitor of
 CC tumour-associated NP-1 dependent angiogenesis. The NPB of the invention
 CC is useful for detecting NP-1 expression, modulation of NP-1 function,
 CC particularly modulation or inhibition of NP-dependent invasion or
 CC adhesion of cells, preferably tumour cells. It is useful in the
 CC manufacture of medicament for the treatment or prevention of NP-dependent
 CC angiogenesis and non-physiological blood vessel growth, particularly
 CC correlated with a tumour. It is also useful for treatment or prevention
 CC of cancer and/or metastasis of tumour cells. The current sequence
 CC represents a single chain antibody neuropilin binder (NPB) polypeptide.
 CC XX
 CC SQ Sequence 613 AA;
 CC XX
 CC SQ Sequence 247 AA;

Query Match 100.0%; Score 92; DB 8; Length 613;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Query Match 95.7%; Score 88; DB 8; Length 247;
 Best Local Similarity 94.1%; Pred. No. 3.8e-05;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDDTIYSPSFQG 17
 Db 69 IIYPGDSDDTIYSPSFQG 85

RESULT 7
 ADR28066 ID ADR28066 standard; protein: 247 AA.
 AC ADR28066;
 XX XX Human anti-TIMP-1 Fab VLCDR3 #48.
 AC ID ABR01560 standard; peptide: 17 AA.
 DT XX Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3;
 DE XX matrix metalloprotease; NMP; variable heavy chain; VLCDR3; hepatotropic;
 KW XX variable light chain; cytosolic; nephrotropic; cardiac; liver fibrosis;
 KW XX alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
 KW XX lupus nephritis; glomerulosclerotic renal disease; lung cancer;
 KW XX idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.
 OS Homo sapiens.

Location/Qualifiers
 Key 89...105
 PT /note= "complementary determining region claimed under
 PT claim 5".
 PT

XX WO200286085-A2.
 XX PN 10-JUL-2002; 2002WO-EP007671.
 XX PR 10-JUL-2001; 2001IT-RM00408.
 XX PD 31-OCT-2002.
 XX PP 24-APR-2002; 2002WO-US012801.
 XX PA (UNIV NAPOLI STUDI FEDERICO II.
 XX PR 24-APR-2001; 2001US-0285683P.
 XX PI D'alessio G, Piccoli R, De Lorenzo C, Palmer DB, Ritter MA;
 XX DR WPI; 2003-221720/21.
 XX N-PDB; ABX12974.
 XX PT New recombinant single-chain anti-ErbB2 antibody of human origin, useful
 PT for pharmaceutical and diagnostic use, and as an antitumor agent for
 PT mammary, ovarian, colon, lung carcinomas, salivary gland or gastric
 PT tumors.
 XX PS Claim 10; Page 8; 47pp; English.
 XX PT The invention discloses a recombinant single-chain anti-ErbB2 antibody of
 PT human origin able to inhibit growth of cells expressing the ErbB2
 PT receptor, referred to as Erbixin. The ErbB2 transmembrane tyrosine kinase
 CC receptor, referred to as Erbixin. The ErbB2 transmembrane tyrosine kinase
 CC receptor (RTK) is highly expressed in breast, ovary and lung carcinomas
 CC as well as salivary gland or gastric tumours. The antibodies new
 CC proteins, nucleotide sequences (gene therapy) and bacteriophage are
 CC useful for pharmaceutical and diagnostic use, and as an antitumor agent,
 CC where the tumour can be mammary, ovarian, colon, lung carcinoma.
 CC salivary gland or gastric tumours. They are also useful in preparing
 CC antiproliferative and antitumour drugs. The sequences presented are the
 CC nucleic acids and encoded polypeptides that were used in the invention to
 CC create the antibody
 XX SQ Sequence 17 AA;
 XX Query Match 92.4%; Score 85; DB 6; Length 17;
 XX Best Local Similarity 94.1%; Pred. No. 7.1e-06;
 XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX ID ADD5218 Standard; peptide; 17 AA.
 XX AC ADD69218;
 XX DT 15-JAN-2004 (first entry)
 XX XX Human heavy chain variable region CDR2 peptide - SEQ ID 22.
 XX DE monoclonal antibody; heavy chain variable region; light; framework;
 XX ID complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
 XX AC prostate specific membrane antigen; PSMA; cytostatic; tumour;
 XX KW Colon cancer; renal carcinoma; gene therapy; human.
 XX OS Homo sapiens.
 XX PN WO2003064406-A2.
 XX PD 07-AUG-2003.
 XX PR 28-JAN-2003; 2003WO-US002448.
 XX PI Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
 XX XX DR WPI; 2003-618360/58.
 XX PT (MEDAREX INC.
 XX PI Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
 XX XX DR WPI; 2003006509-A2.
 XX PN WO2003006509-A2.
 XX PD 23-JAN-2003.

XX WO200286085-A2.
 XX PN 10-JUL-2002; 2002WO-EP007671.
 XX PR 10-JUL-2001; 2001IT-RM00408.
 XX PD 31-OCT-2002.
 XX PP 24-APR-2002; 2002WO-US012801.
 XX PA (UNIV NAPOLI STUDI FEDERICO II.
 XX PR 24-APR-2001; 2001US-0285683P.
 XX PI D'alessio G, Piccoli R, De Lorenzo C, Palmer DB, Ritter MA;
 XX DR WPI; 2003-221720/21.
 XX N-PDB; ABX12974.
 XX PT New recombinant single-chain anti-ErbB2 antibody of human origin, useful
 PT for pharmaceutical and diagnostic use, and as an antitumor agent for
 PT mammary, ovarian, colon, lung carcinomas, salivary gland or gastric
 PT tumors.
 XX PS Claim 10; Page 8; 47pp; English.
 XX PT The invention discloses a recombinant single-chain anti-ErbB2 antibody of
 PT human origin able to inhibit growth of cells expressing the ErbB2
 PT receptor, referred to as Erbixin. The ErbB2 transmembrane tyrosine kinase
 CC receptor, referred to as Erbixin. The ErbB2 transmembrane tyrosine kinase
 CC receptor (RTK) is highly expressed in breast, ovary and lung carcinomas
 CC as well as salivary gland or gastric tumours. The antibodies new
 CC proteins, nucleotide sequences (gene therapy) and bacteriophage are
 CC useful for pharmaceutical and diagnostic use, and as an antitumor agent,
 CC where the tumour can be mammary, ovarian, colon, lung carcinoma.
 CC salivary gland or gastric tumours. They are also useful in preparing
 CC antiproliferative and antitumour drugs. The sequences presented are the
 CC nucleic acids and encoded polypeptides that were used in the invention to
 CC create the antibody
 XX SQ Sequence 17 AA;
 XX Query Match 92.4%; Score 85; DB 6; Length 17;
 XX Best Local Similarity 94.1%; Pred. No. 7.1e-06;
 XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX ID ADD5218 Standard; peptide; 17 AA.
 XX AC ADD69218;
 XX DT 15-JAN-2004 (first entry)
 XX XX Human heavy chain variable region CDR2 peptide - SEQ ID 22.
 XX DE monoclonal antibody; heavy chain variable region; light; framework;
 XX ID complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
 XX AC prostate specific membrane antigen; PSMA; cytostatic; tumour;
 XX KW Colon cancer; renal carcinoma; gene therapy; human.
 XX OS Homo sapiens.
 XX PN WO2003064406-A2.
 XX PD 07-AUG-2003.
 XX PR 28-JAN-2003; 2003WO-US002448.
 XX PI Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
 XX XX DR WPI; 2003-618360/58.
 XX PT (MEDAREX INC.
 XX PI Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
 XX XX DR WPI; 2003006509-A2.
 XX PN WO2003006509-A2.
 XX PD 23-JAN-2003.

XX WO200286085-A2.
 XX PN 10-JUL-2002; 2002WO-EP007671.
 XX PR 10-JUL-2001; 2001IT-RM00408.
 XX PD 31-OCT-2002.
 XX PP 24-APR-2002; 2002WO-US012801.
 XX PA (UNIV NAPOLI STUDI FEDERICO II.
 XX PR 24-APR-2001; 2001US-0285683P.
 XX PI D'alessio G, Piccoli R, De Lorenzo C, Palmer DB, Ritter MA;
 XX DR WPI; 2003-221720/21.
 XX N-PDB; ABX12974.
 XX PT New recombinant single-chain anti-ErbB2 antibody of human origin, useful
 PT for pharmaceutical and diagnostic use, and as an antitumor agent for
 PT mammary, ovarian, colon, lung carcinomas, salivary gland or gastric
 PT tumors.
 XX PS Claim 10; Page 8; 47pp; English.
 XX PT The invention discloses a recombinant single-chain anti-ErbB2 antibody of
 PT human origin able to inhibit growth of cells expressing the ErbB2
 PT receptor, referred to as Erbixin. The ErbB2 transmembrane tyrosine kinase
 CC receptor, referred to as Erbixin. The ErbB2 transmembrane tyrosine kinase
 CC receptor (RTK) is highly expressed in breast, ovary and lung carcinomas
 CC as well as salivary gland or gastric tumours. The antibodies new
 CC proteins, nucleotide sequences (gene therapy) and bacteriophage are
 CC useful for pharmaceutical and diagnostic use, and as an antitumor agent,
 CC where the tumour can be mammary, ovarian, colon, lung carcinoma.
 CC salivary gland or gastric tumours. They are also useful in preparing
 CC antiproliferative and antitumour drugs. The sequences presented are the
 CC nucleic acids and encoded polypeptides that were used in the invention to
 CC create the antibody
 XX SQ Sequence 17 AA;
 XX Query Match 92.4%; Score 85; DB 6; Length 17;
 XX Best Local Similarity 94.1%; Pred. No. 7.1e-06;
 XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX ID ADD5218 Standard; peptide; 17 AA.
 XX AC ADD69218;
 XX DT 15-JAN-2004 (first entry)
 XX XX Human heavy chain variable region CDR2 peptide - SEQ ID 22.
 XX DE monoclonal antibody; heavy chain variable region; light; framework;
 XX ID complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
 XX AC prostate specific membrane antigen; PSMA; cytostatic; tumour;
 XX KW Colon cancer; renal carcinoma; gene therapy; human.
 XX OS Homo sapiens.
 XX PN WO2003064406-A2.
 XX PD 07-AUG-2003.
 XX PR 28-JAN-2003; 2003WO-US002448.
 XX PI Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
 XX XX DR WPI; 2003-618360/58.
 XX PT (MEDAREX INC.
 XX PI Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
 XX XX DR WPI; 2003006509-A2.
 XX PN WO2003006509-A2.
 XX PD 23-JAN-2003.

XX

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Query Match      92.4%; Score 85; DB 8; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy   1 I I Y P O D S D T I Y S P S E Q 17
Dn   1 I T Y P E D S D T R Y S P S Q G 17

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Total time: 20.075 seconds

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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:11:59 ; Search time 4.64898 Seconds
351.837 Million cell updates/sec (without alignments)

Title: US-10-769-144-14
Perfect score: 92
Sequence: 1 ILYPGDSDTIYSPSFQG 17

Scoring table: BLOSUM62
GapOp 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : PIR 80:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	92.4	98	2 PH1274	19 heavy chain V r
2	85	92.4	98	2 S26907	19 heavy chain V r
3	85	92.4	101	2 S12428	19 heavy chain V r
4	85	92.4	101	2 S12424	19 heavy chain V r
5	85	92.4	102	2 PH1266	19 heavy chain V r
6	85	92.4	102	2 PH1279	19 heavy chain V r
7	85	92.4	102	2 PH1281	19 heavy chain V r
8	85	92.4	102	2 PH1277	19 heavy chain V r
9	85	92.4	102	2 PH1244	19 heavy chain V r
10	85	92.4	102	2 PH1267	19 heavy chain V r
11	85	92.4	102	2 PH1272	19 heavy chain V r
12	85	92.4	102	2 PH1282	19 heavy chain V r
13	85	92.4	102	2 PH1248	19 heavy chain V r
14	85	92.4	102	2 PH1280	19 heavy chain V r
15	85	92.4	102	2 PH1258	19 heavy chain V r
16	85	92.4	102	2 PH1264	19 heavy chain V r
17	85	92.4	102	2 PH1259	19 heavy chain V r
18	85	92.4	102	2 PH1273	19 heavy chain V r
19	85	92.4	102	2 PH1249	19 heavy chain V r
20	85	92.4	102	2 PH1271	19 heavy chain V r
21	85	92.4	102	2 PH1278	19 heavy chain V r
22	85	92.4	104	2 B36006	19 heavy chain V r
23	85	92.4	113	2 PH1428	19 heavy chain V r
24	85	92.4	115	2 PH1557	19 heavy chain V r
25	85	92.4	117	2 A26846	19 heavy chain pre
26	85	92.4	117	2 S19670	19 heavy chain V r
27	85	92.4	123	2 PH1423	19 heavy chain V r
28	85	92.4	123	2 S38492	19 heavy chain - h
29	85	92.4	123	2 C36006	19 heavy chain V r

ALIGNMENTS

RESULT 1							
PH1274	19 heavy chain V region (clone PB15) - human (fragment)	C;Species: Homo sapiens (man)	C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996	C;Accession: PH1274	R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.	J. Exp. Med. 176, 1073-1081, 1992	A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
		A;Cross-references: UNIPARC:UPI000017683F			A;Reference number: PH1232; PMID:93018822;	A;Accession: PH1274	C;Superfamily: immunoglobulin V region; immunoglobulin C;Keywords: heterotetramer; immunoglobulin A;Molecule type: DNA A;Residues: 1-98 <CAI>
Query	1 IIYPGDSDTIYSPSFQG 17	Query Match	92.4%;	Score 85;	DB 2;	Length 98;	
		Best Local Similarity	94.1%;	Pred. No.	1.3e-06;	Mismatches 0;	Gaps 0;
Db	54 IIYPGDSDTIYSPSFQG 70	Matches 16;	Conservative 0;	Indels 0;			

RESULT 2							
S26907	19 heavy chain V region (DP-73) - human	C;Species: Homo sapiens (man)	C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999	C;Accession: S26907	R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.	J. Mol. Biol. 227, 776-798, 1992	A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of v A;Reference number: S26885; PMID:93021117; PMID:1404388
		A;Cross-references: UNIPARC:UPI00011641B; EMBL:212373; PIDN:932965; PIDN:CAA78243.1; PID					C;Superfamily: immunoglobulin V region; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F=15-98/Domain: immunoglobulin homology <IMM>
Query	92.4%;	Score 85;	DB 2;	Length 98;			
Db	54 IIYPGDSDTIYSPSFQG 17	Best Local Similarity	94.1%;	Pred. No.	1.3e-06;	Mismatches 1;	Gaps 0;
		Matches 16;	Conservative 0;	Indels 0;			

Db 50 IIYPGDSDTRYSPSPFQG 66

RESULT 3
 S12428 Ig heavy chain V region (5JB) - human
 C;Species: Homo sapiens (man)
 C;Accession: S12428
 R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Capra, J.D.
 EMBL J. 8 3741-3748, 1989
 A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
 A;Reference: number: S09421; MUID:90059975; PMID:2511001
 A;Accession: S12428
 A;Status: preliminary; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-101 <SAN>
 A;Cross-references: UNIPARC:UPI0000176BB; EMBL:X56367
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;18-101/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 101;
 Best Local Similarity 94.1%; Pred. No. 1.3e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSPFQG 17
 Db 53 IIYPGDSDTRYSPSPFQG 69

RESULT 5
 PH1266 Ig heavy chain V region (Clone VERB5) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C;Accession: PH1266
 R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
 J. Exp. Med. 176, 1073-1081, 1992
 A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
 A;Reference number: PH1232; MUID:93018822; PMID:1402653
 A;Accession: PH1266
 A;Molecule type: mRNA
 A;Residues: 1-102 <CAI>
 A;Cross-references: UNIPARC:UPI0000176BD2
 A;Experimental source: adult PBL
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
 Best Local Similarity 94.1%; Pred. No. 1.3e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSPFQG 17
 Db 54 IIYPGDSDTRYSPSPFQG 70

RESULT 6
 PH1279 Ig heavy chain V region (clones CH11, CORD3, CORD4, CORD8, CORD9, CD+1, CD+3, CD+4, CD+9) - human
 C;Species: Homo sapiens (man)
 C;Accession: PH1279 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C;Accession: PH1279
 R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
 J. Exp. Med. 176, 1073-1081, 1992
 A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
 A;Reference number: PH1232; MUID:93018822; PMID:1402653
 A;Accession: PH1279
 A;Molecule type: DNA
 A;Residues: 1-102 <CAI>
 A;Cross-references: UNIPARC:UPI0000116D01
 A;Experimental source: adult PBL
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
 Best Local Similarity 94.1%; Pred. No. 1.3e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSPFQG 17
 Db 54 IIYPGDSDTRYSPSPFQG 70

RESULT 7
 PH1281 Ig heavy chain V region (Clone PB112) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Accession: PH1281
 R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
 J. Exp. Med. 176, 1073-1081, 1992
 A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
 A;Reference number: PH1232; MUID:93018822; PMID:1402653
 A;Accession: PH1281
 A;Molecule type: DNA
 A;Residues: 1-101 <SA6>
 A;Cross-references: UNIPARC:UPI000011636C; EMBL:X56371
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-101 <SA4>
 A;Cross-references: UNIPARC:UPI000011636C; EMBL:X56368
 A;Accession: S12429
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-101 <SA5>
 A;Cross-references: UNIPARC:UPI000011636C; EMBL:X56369
 A;Accession: S12432
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-101 <SA6>
 A;Cross-references: UNIPARC:UPI000011636C; EMBL:X56371
 C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Accession: PH1281
 R.;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
 J.; Exp. Med. 176, 1073-1081, 1992
 A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
 A;Reference number: PH1232; MUID:93018822; PMID:1402653
 A;Accession: PH1281
 A;Molecule type: DNA
 A;Residues: 1-102 <CAI>
 A;Cross-references: UNIPARC:UPI0000176C57
 A;Experimental source: adult PBL
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
 Best Local Similarity 94.1%; Pred. No. 1.3e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIFYPGDSDTIVYSPSFQG 17
 Db 54 IIFYPGDSDTIVYSPSFQG 70

RESULT 8
 PH1277
 Ig heavy chain V region (clone PBL8) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C;Accession: PH1277
 R.;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
 J.; Exp. Med. 176, 1073-1081, 1992
 A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
 A;Reference number: PH1232; MUID:93018822; PMID:1402653
 A;Accession: PH1277
 A;Molecule type: DNA
 A;Residues: 1-102 <CAI>
 A;Cross-references: UNIPARC:UPI0000176B41
 A;Experimental source: adult PBL
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
 Best Local Similarity 94.1%; Pred. No. 1.3e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIFYPGDSDTIVYSPSFQG 17
 Db 54 IIFYPGDSDTIVYSPSFQG 70

RESULT 9
 PH1244
 Ig heavy chain V region (clone CORD2) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C;Accession: PH1244
 R.;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
 J.; Exp. Med. 176, 1073-1081, 1992
 A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
 A;Reference number: PH1232; MUID:93018822; PMID:1402653
 A;Accession: PH1244
 A;Molecule type: DNA
 A;Residues: 1-102 <CAI>
 A;Cross-references: UNIPARC:UPI0000176BC8
 A;Experimental source: cord blood B cell
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
 Best Local Similarity 94.1%; Pred. No. 1.3e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Cross-references: UNIPARC:UPI0000176068
C;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches -1; Indels 0; Gaps 0;
A;Accession: PH1258
A;Cross-references: UNIPARC:UPI0000176BCD
A;Experimental source: cord blood B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

RESULT 13
PH1248
IG heavy chain V region (clone CORD6) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1248
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1248
A;Cross-references: UNIPARC:UPI0000176A4E
A;Residue: 1-102 <CAI>
A;Molecule type: DNA
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches -1; Indels 0; Gaps 0;
A;Accession: PH1248
A;Cross-references: UNIPARC:UPI0000176A4E
A;Residue: 1-102 <CAI>
A;Molecule type: DNA
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches -1; Indels 0; Gaps 0;
A;Accession: PH1248
A;Cross-references: UNIPARC:UPI0000176BCD
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches -1; Indels 0; Gaps 0;
A;Accession: PH1258
A;Cross-references: UNIPARC:UPI0000176068
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	Q4n6s9 theileria p
OM protein - protein search, using sw model		Q9xz24_drosophila
Run on:	December 3, 2005, 14:11:48 ; Search time 29.9755 Seconds (without alignments) 400.126 Million cell updates/sec	Q54nu3 dictyosteli
Title:	US-10-769-144-14	P98157 gallus galli
Perfect score:	92	Q92553 mus musculu
Sequence:	I IYPGDSDTIYSPSFQG 17	Q6fsy9 candida gla
Scoring table:	BLOSUM62	P15110 burkholderi
Gapop:	10.0 , Gapext 0.5	Q4lv17_bURK
Searched:	2166443 seqs, 705528306 residues	Q9rvn0_deirka
Total number of hits satisfying chosen parameters:	2166443	Q61rc1 canorhabdi
Minimum DB seq length: 0		P0a058 staphylloc
Maximum DB seq length: 2000000000		P21867 escherichia
Post-processing: Minimum Match 0%		Q7ux12 rhoopirell
Maximum Match 100%		HIS82_cau R acter
Mus musculus (Mouse)		Q9asb6 cau R acter
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC		
OC Muroidea; Muridae; Murinae; Mus;		
OX NCBI TaxID=1050;		
[1]		RN
NUCLEOTIDE SEQUENCE.		RP
STRAIN=CZBCH II;		RC
TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;		RC
ID Q8R316_MOUSE PRELIMINARY;		RC
AC Q8R316;		RC
DT 01-JUN-2002 (TREMBLref. 21, Created)		RC
DT 01-JUN-2002 (TREMBLref. 21, Last sequence update)		RC
DT 01-MAR-2004 (TREMBLref. 26, Last annotation update)		RC
DE Igfb Protein.		RC
GN Name=lgfb; Synonyms=AU044919;		RA
OS Mus musculus (Mouse).		RA
RA Klaunser R.D., Collins F.S., Wagner L., Shemer C.M., Schuler G.D.,		RA
RA Altschul S.P., Zabeck B., Buetz K.H., Grouse L.H., Derge J.G.,		RA
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		RA
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		RA
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		RA
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		RA
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulahay S.J.,		RA
RA Bosak S.A., McEvans P.J., McKernan K.J., Malek J.A., Guarnatne P.H.,		RA
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		RA
RA Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		RA
RA Pahey J., Helton B., Ketteman M., Madan A.J., Rodrigues S., Sanchez A.,		RA
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		RA
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		RA
RA Rodriguez A.C.N., Grimwood J.J., Schmutz J., Myers R.M.,		RA
RA Butcher D.Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,		RA
RA Schnarch A., Schein J.E., Jones S.J.M., Marrs M.A.; RT "Generation and initial analysis of more than 15,000 full-length human		RA
RT and mouse cDNA sequences";		RT
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		RL
NUCLEOTIDE SEQUENCE.		RN
STRAIN=CZBCH II;		RP
TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;		RC
Director MGC Project;		RC
Submitted (MAR-2002) to the ENSEMBL/GenBank/DBDBJ databases.		RL
EMBL; BC02447; AAH25447.1; -; mRNA.		DR
HSSP; P01859; 1CL7.		DR
SMR; Q8R31H6; 20-470.		DR
MG1; MG1:2144967; AU044919.		DR
GO; GO:0003823; F: antigen binding; IEA.		DR
InterPro; IPR07110; Ig-like.		DR
InterPro; IPR003597; Ig-cl.		DR
InterPro; IPR003006; Ig_MHC.		DR

DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS05035; Ig_LIKE; 5.
 DR PROSITE; PS00290; Ig_MHC; UNKNOWN_3.
 KW Immunoglobulin domain.
 SQ SEQUENCE 614 AA; MW: 839BAF3BBD124F89 CRC64;
 Query Match Score 56; DB 2; Length 614;
 Best Local Similarity 56.2%; Pred. No. 3.5%;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 RN NUCLEOTIDE SEQUENCE.
 Q9JL83 MOUSE PRELIMINARY; PRT; 110 AA.
 ID Q9JL83_MOUSE PRELIMINARY;
 AC Q9JL83;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Anti-myosin immunoglobulin heavy chain variable region
 (Fragment).
 OS Mus musculus (Mouse).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 STRAIN=BALB/C;
 RX MEDLINE=0448342; PubMed=109924488;
 RX DOI=10.1128/IAI.68.10.5803-5808.2000;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "T-Cell-dependent antibody response to the dominant epitope of
 streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
 with cardiac myosin.";
 RL Infect. Immun. 68:5803-5808 (2000).
 EMBL; AP26022; AAH69321.1; -; mRNA.
 HSSP; P01751; 1NQB.
 SMR; Q9JL83; 1-110.
 DR Ensemble; ENSMUSG00000063520; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS05035; Ig_LIKE; 1.
 FT NON_TER 1 1
 FT NON_TER 110 110
 SQ SEQUENCE 110 AA; MW: 84E6F2AD219AF95B CRC64;
 Query Match Score 56.7%; DB 2; Length 110;
 Best Local Similarity 56.2%; Pred. No. 1;
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 RN NUCLEOTIDE SEQUENCE.
 Q9JL83 MOUSE PRELIMINARY; PRT; 120 AA.
 ID Q9JL83_MOUSE PRELIMINARY;
 AC Q9JL83;
 DT 01-DBC-2001 (TREMBLrel. 19, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DB IgV-J558 protein.
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 STRAIN=FVB/N; TISSUE=Colon;
 ID Q91W11_MOUSE PRELIMINARY;
 AC Q91W11;
 DT 01-DBC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DB IgV-J558 protein.
 OS Mus musculus (Mouse).
 RA Klausner R.D., Colling F.S., Wagner J., Shemesh C.M., Schuler G.D.,
 RA Altchul S.F., Zeeberg B., Buetow K.H., Scheuer C.F., Bhat N.K.,
 RA Villalobos D.K., Muzny D.M., Sodergren E.J., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Schaetz T.B.,
 RA Brownstein M.J., Uedin T.B., Yoshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Louieell N.A., Peters G.J., Abramson R.D., Mullisby S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faney J., Heilcon E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green R.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska D.T., Smalius D.E.,
 RA Schein J.E., Jones S.J.M., Marrs M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RA Strausberg R.;

RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; BC013490; AAH13490_1.; - ; mRNA.

DR HSSP; P01751; 1A6W.

DR Ensemble: ENSMUSG000000211555; Mus musculus.

DR GO; GO:0003823; F:antigen binding; IEA.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR001597; Ig_C1.

DR InterPro; IPR00306; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam: PF07654; C1-set; 2.

DR SMART; SM0046; IgV; 1.

DR PROSITE; PS50835; Ig_LIKE; 4.

DR PROSITE; PS000290; Ig_MHC; UNKNOWN_2.

KW Immunoglobulin domain.

SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 57.6%; Score 53; DB 2; Length 481;

Best Local Similarity 56.2%; Pred. No. 8.2;

Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IYPGDSPTIYSFPSFQG 17

Db 70 IYPGDSPTIYSFPSFQG 85

RESULT 9
HV52 MOUSE . STANDARD; PRT; 117 AA.

AC P06327; 06 , Created)

DT 01-JAN-1988 (Rel. 06 , Last sequence update)

DT 01-MAY-2005 (Rel. 4 , Last annotation update)

DB Ig heavy chain V region VH558 A1/A4 precursor.

OS Mus musculus (Mouse).

OC Bacteria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Gires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

RN [1] NCBI_TaxID=10090;

RP NUCLEOTIDE SEQUENCE.

STRAIN=FVB/N;

RC TISSUE=Mammary tumor. Metallothionein-TGF alpha model. 10 month old

RC virgin mouse. Taken by biopsy.; PRT; 463 AA.

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.P., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshinyan S., Garniuci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malik J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smialius D.E.,

RA Scheiner A., Schein J.E., Jones S.J.M., Marra M.A.;

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC DR EMBL; M13787; AAA38599.1.; - ; mRNA.

DR PIR; A02029; HWSM1.

DR HSSP; P01820; 1G7J.

DR PROSITE; PS50835; Ig_LIKE; 1.

KW Immunoglobulin domain; Immunoglobulin V region; signal.

FT SIGNAL 1 19 Ig heavy chain V region VH558 A1/A4.

FT CHAIN 20 117 Framework-1.

FT REGION 20 49 Complementarity-determining-1.

FT REGION 50 54 Framework-2.

FT REGION 55 68 Complementarity-determining-2.

FT REGION 69 85 Framework-3.

FT DISULFD 86 117 By similarity.

FT NON_TER 41 115

FT SEQUENCE 117 117

Query Match 56.5%; Score 52; DB 1; Length 117;

RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; BC013490; AAH13490_1.; - ; mRNA.

DR HSSP; P01751; 1A6W.

DR Ensemble: ENSMUSG000000211555; Mus musculus.

DR GO; GO:0003823; F:antigen binding; IEA.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR001597; Ig_C1.

DR InterPro; IPR00306; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam: PF07654; C1-set; 2.

DR SMART; SM0046; IgV; 1.

DR PROSITE; PS50835; Ig_LIKE; 4.

KW Immunoglobulin domain.

SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 57.6%; Score 53; DB 2; Length 481;

Best Local Similarity 56.2%; Pred. No. 2.3;

Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IYPGDSPTIYSFPSFQG 17

Db 70 IYPGDSPTIYSFPSFQG 85

RESULT 10
Q99LC4_MOUSE . PRELIMINARY; PRT; 463 AA.

AC Q99LC4;

DT 01-JUN-2001 (TREMBUREL. 17, Created)

DT 01-JUN-2001 (TREMBUREL. 17, Last annotation update)

DT 01-MAR-2004 (TREMBUREL. 26, Last annotation update)

DB Ig-4 protein.

GN Name-Ig-4;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Gires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

RN [1] NCBI_TaxID=10090;

RP NUCLEOTIDE SEQUENCE.

STRAIN=FVB/N;

RC TISSUE=Mammary tumor. Metallothionein-TGF alpha model. 10 month old

RC virgin mouse. Taken by biopsy.; PRT; 463 AA.

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.P., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshinyan S., Garniuci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malik J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,

RA RAFAELSON D.K., MUZNY D.M., SODERGREN E.J., LU X., GIBBS R.A.,

RA FAHEY J., HELTON E., KETTEMAN M., MADAN A., RODRIGUES S., SANCHEZ A.,

RA WHITING M., MADAN A., YOUNG A.C., BOUFFARD G.G.,

RA BLAKESLEY R.W., TOUCHMAN J.W., GREEN E.D., DICKSON M.C.,

RA RODRIGUEZ A.C., GRIMWOOD J., SCHMUTZ J., MYERS R.M.,

RA BUTTERFIELD Y.S.N., KRZYWINSKI M.J., SKALSKA U., SMAILIAS D.E.,

RA RAUCHER A., SCHEIN J.E., JONES S.J.M., MARZA M.A.;

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CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC DR EMBL; M13787; AAA38599.1.; - ; mRNA.

DR PIR; A02029; HWSM1.

DR HSSP; P01820; 1G7J.

DR PROSITE; PS50835; Ig_LIKE; 1.

KW Immunoglobulin domain; Immunoglobulin V region; signal.

FT SIGNAL 1 19 Framework-1.

FT CHAIN 20 49 Complementarity-determining-1.

FT REGION 50 54 Framework-2.

FT REGION 55 68 Complementarity-determining-2.

FT REGION 69 85 Framework-3.

FT DISULFD 86 117 By similarity.

FT NON_TER 117 117

FT SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 56.5%; Score 52; DB 1; Length 117;

DR	InterPro; IPR003597; Ig_c1.			
DR	Pfam; PF003596; Ig_v.			
DR	SMART; SM00406; Ig_v_1.			
DR	PROSITE; PS050835; Ig_LIKE;	4.		
KW	Immunoglobulin domain.			
SQ	SEQUENCE 463 AA; 51008 MW; EAA674C6BBC30783 CRC64;			
Query Match	56 5%; Score 52; DB 2; Length 463;			
Best Local Similarity	56.2%; Pred. No. 11;			
Matches	9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
Qy	2 IYPGDSDTTSPSPFOG 17			
Db	70 IYPGSNTYSEKFKG 85			
RESULT 11				
HV06_MOUSE	ID_HV06 MOUSE STANDARD; PRT; 117 AA.			
AC	PO17E0 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	20-MAY-2005 (Rel. 47, Last annotation update)			
DE	19 heavy chain V region 102 precursor.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Bucerotidae; Bucohontoglires; Glires; Rodentia; Sciurognathini; Muridae; Muridae; Murinae; Mus.			
NCBI_TAXID	10090; NCBI_TAXID=10090; KINESINHEAVY.			
RN				
RP	NUCLEOTIDE SEQUENCE.			
STRAIN_C57BL/6J	PROSITE; PS00011; KINESIN_MOTOR_DOMAIN1; 1.			
RX	PROSITE; PS00067; KINESIN_MOTOR_DOMAIN2; 1.			
MEDLINE=81234548; PubMed=6788276; DOI=10.1016/0092-8674(81)90089-1; Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K., Baltimore D.; "Heavy chain variable region contribution to the Npb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:655-637(1981); -1 - MISCELLANEOUS: This germline gene belongs to a set of closely related genes that could encode V regions of Npb antibodies.	ATP-binding; Microtubule; Motor protein; Nucleotide-binding.			
CC	CC	CC	CC	CC
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.	SEQUENCE 90 AA; 100815 MW; 424E3CDF67BDF4F CRC64;	Query Match	55 4%; Score 51; DB 2; Length 909; Best Local Similarity 64.3%; Pred. No. 36; Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
CC			Qy	4 PGDSTTIYSPSFOG 17
CC			Db	115 PGTSDFGYSPEFRG 128
RESULT 13				
Q4H3H2_C10IN	ID_Q4H3H2_C10IN PRELIMINARY; PRT; 193 AA.			
AC	Q4H3H2_			
DT	13-SEP-2005 (TREMBLrel. 31, Created)			
DT	13-SEP-2005 (TREMBLrel. 31, Last sequence update)			
DT	13-SEP-2005 (TREMBLrel. 31, Last annotation update)			
DB	Fringe (Fragment).			
GN	Name-Ci-Fringe 4; Ciona intestinalis.			
OS	Ciona intestinalis.			
OC	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiaceae; Enterogona; Phleobranchia; Clionidae; Ciona.			
OX	NCBI_TAXID=7719;			
RN				
RP	NUCLEOTIDE SEQUENCE.			
DR	Ensembl; ENSMISG00000062849; Mus musculus.			
DR	InterPro; IPR007110; Ig-like.			
DR	SMART; SM00406; Ig_v_1.			
DR	PROSITE; PS050835; Ig_LIKE;	1.		
KW	3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.			
SQ	SIGNAL 1 19	Ig heavy chain V region 102.		
PT	CHAIN 20 117	Framework-1.		
PT	REGION 20 49	Complementarity-determining-1.		
PT	REGION 50 54	Framework-2.		
PT	REGION 55 68	Complementarity-determining-2.		
PT	REGION 69 85	Framework-3.		
PT	REGION 86 117	By similarity.		
PT	DISULPID 41 115			
PT	NON_TER 117 117			
SQ	SEQUENCE 117 AA; 12867 MW; 740A65DD851FC8C CRC64;			
Query Match	55.4%; Score 51; DB 1; Length 117;			
Best Local Similarity	56.2%; Pred. No. 3.4;			
Matches	9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;			
Qy	2 IYPGDSDTTSPSPFOG 17			

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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:24:58 ; Search time 7.21633 Seconds
 (without alignments)
 194.765 Million cell updates/sec

Title: US-10-769-144-14

Perfect score: 92

Sequence: IIRYPGDSDTIYSFSPFQG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:/*
 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:/*
 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:/*
 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:/*
 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:/*
 6: /cgn2_6/ptodata/1/iaa/backfile1.pep:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

RESULT 1
 US-10-769-039-81
 ; Sequence 81, Application US/08478039
 ; Patent No. 5681722

GENERAL INFORMATION:

APPLICANT: Newman, Roland A.
 APPLICANT: Hanna, Nabil
 APPLICANT: Raab, Ronald W.
 TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
 NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 STREET: 699 Prince St.
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,039
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIORITY NUMBER: US 08/379,072

APPLICATION NUMBER: US 08/379,072
 FILING DATE: 25-JAN-1995
 PRIORITY NUMBER: US 07/912,292

APPLICATION NUMBER: US 07/912,292
 FILING DATE: 10-JUL-1992
 PRIORITY NUMBER: US 07/856,281

APPLICATION NUMBER: US 07/856,281
 FILING DATE: 23-MAR-1992
 PRIORITY NUMBER: US 07/735,064

APPLICATION NUMBER: US 07/735,064
 FILING DATE: 25-JUL-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Teskin Esq., Robin L.
 REGISTRATION NUMBER: 35,030
 REFERENCE/DOCKET NUMBER: 012712-160

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620
 TELEFAX: 703-836-2011
 INFORMATION FOR SEQ ID NO: 81:

SEQUENCE CHARACTERISTICS:
 LENGTH: 98 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant

Result No.	Score	Query Match	Length	DB ID	Description
1	85	92.4	98	1	US-08-478-039-81
2	85	92.4	98	1	US-08-478-039-81
3	85	92.4	98	1	US-08-665-202-50
4	85	92.4	98	2	US-09-315-574-45
5	85	92.4	98	2	US-09-315-574-46
6	85	92.4	111	2	US-09-315-574-47
7	85	92.4	111	2	US-09-315-574-48
8	85	92.4	117	2	US-08-315-574-49
9	85	92.4	117	2	US-09-315-574-50
10	85	92.4	119	2	US-09-315-574-51
11	85	92.4	119	2	US-09-490-0704-26
12	85	92.4	119	2	US-09-490-153-26
13	85	92.4	119	2	US-09-490-153-40
14	85	92.4	120	2	US-09-490-153-67
15	85	92.4	120	2	US-09-025-769B-40
16	85	92.4	120	2	US-09-025-769B-67
17	85	92.4	120	2	US-09-490-0704-40
18	85	92.4	120	2	US-09-490-153-26
19	85	92.4	120	2	US-09-490-153-40
20	85	92.4	120	2	US-09-490-324-40
21	85	92.4	120	2	US-09-490-324-67
22	84	91.3	125	1	US-08-665-202-56
23	84	91.3	125	1	US-09-315-574-56
24	83	90.2	125	1	US-08-665-202-44
25	83	90.2	125	1	US-08-665-202-45
26	83	90.2	125	1	US-08-665-202-46
27	83	90.2	125	1	US-08-665-202-47

TOPOLGY: not relevant
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE: peptide
 ORGANISM: Homo sapiens
 POSITION IN GENOME:
 CHROMOSOME SEGMENT: VHS consensus
 US-08-478-039-81

Query Match 92.4%; Score 85; DB 1; Length 98;
 Best Local Similarity 94.1%; Pred. No. 2.7e-05;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 I I Y P D S D T I Y S P S F Q 17
 Db 50 I I Y P D S D T R Y S P S F Q 66

RESULT 3
 US-08-665-202-33
 ; Sequence 33, Application US/08665202

US-08-476-349A-81
 ; Sequence 81, Application US/08476349A

GENERAL INFORMATION:
 ; Patent No. 5750105
 ; APPLICANT: Newman, Roland A.
 ; APPLICANT: Hanna, Nabil
 ; APPLICANT: Raab, Ronald W.
 ; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
 ; NUMBER OF SEQUENCES: 114
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: BURNS, DOANE, SWECKER & MATHIS
 ; STREET: 699 Prince St.
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/665,202
 FILING DATE: 13-JUN-1996
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 60/000,238
 FILING DATE: 14-JUN-1995
 PRIORITY APPLICATION NUMBER: US 60/000,250
 FILING DATE: 15-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 38,498
 REFERENCE/DOCKET NUMBER: 02307E-061410
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 33:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 98 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-665-202-33

Query Match 92.4%; Score 85; DB 1; Length 98;
 Best Local Similarity 94.1%; Pred. No. 2.7e-05;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 I I Y P D S D T I Y S P S F Q 17
 Db 50 I I Y P D S D T R Y S P S F Q 66

RESULT 4
 US-09-315-574-33
 ; Sequence 33, Application US/09315574
 ; Patent No. 6512097
 ; GENERAL INFORMATION:

APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: Q2307B-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: Peptide
 -09-315-574-33
 Query Match 92.4%; Score 85; DB 2; Length 98;
 Best Local Similarity 94.1%; Pred. No. 2.7e-05;
 Matches 16; Conservative 0; Mismatches 1; Indels 0;
 Caps 0;

1	I I Y P G D S D T I Y S P S F Q G	17
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RESULT 5
-10-194-975-45
Sequence 45, Application US/10194975
Patent No. 6881557
GENERAL INFORMATION:
APPLICANT: Footh, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,375
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.1
SEQ ID NO 45
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens

US-10-194-975-45

	Query Match Best Local Similarity Matches	Match 16;	Score 92.4%; Conservative	Pred. No. 0.2.7e-05;	DB 2; Mismatches 0;	Length 98;	Gaps 0;
Qy	1	IIPGDSOTIYSPFQG	17				
Db	50	IIPGDSOTIYSPFQG	66				

RESULT 6

	US-09-726-219A-171	US/09726219A
Sequence	171,	Application US/09726219A
Patent No.	6806079	
GENERAL INFORMATION:		
APPLICANT:	Cambridge Antibody Technology Limited	
APPLICANT:	Medical Research Council	
APPLICANT:	McAfferty, John	
APPLICANT:	Pope, Anthony	
APPLICANT:	Johnson, Kevin	
APPLICANT:	Hoogenboom, Hendricus	
APPLICANT:	Griffiths, Andrew	
APPLICANT:	Jackson, Ronald	
APPLICANT:	Holliger, Kasper	
APPLICANT:	Marks, James	
APPLICANT:	Clackson, Timothy	
APPLICANT:	Chiswell, David	
APPLICANT:	Winter, Gregory	
APPLICANT:	Bonart, Timothy	
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs		
FILE REFERENCE:	2138339-00013	
CURRENT APPLICATION NUMBER:	US/09/726,219A	
CURRENT FILING DATE:	2000-11-28	
PRIOR APPLICATION NUMBER:	GB 9015198.6	
PRIOR FILING DATE:	1990-07-10	
PRIOR APPLICATION NUMBER:	GB 9022845.3	
PRIOR FILING DATE:	1990-10-19	
PRIOR APPLICATION NUMBER:	GB 9022845.3	
PRIOR FILING DATE:	1990-10-19	
PRIOR APPLICATION NUMBER:	GB 9024503.6	
PRIOR FILING DATE:	1990-11-12	

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; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 171
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-219A-171

Query Match          92 4%; Score 85; DB 2%; Length 111;
Best Local Similarity 94 1%; Pred. No. 3.1e-05;
Matches 16; Conservative 0; Mismatches -1; Indels 0; Gaps 0
Qy      1 IIVPGDSDTRYSPSPFG 17
Db      50 IIVPGDSDTRYSPSPFG 66

RESULT 7
US-09-196-522-171
; Sequence 171, Application US/09196522

```

```

/*
 * Patent No. 6916605
 * GENERAL INFORMATION:
 *   APPLICANT: Cambridge Antibody Technology
 *   APPLICANT: Cambridge Antibody Technology Limited
 *   APPLICANT: Medical Research Council
 *   APPLICANT: McCafferty, John
 *   APPLICANT: Pope, Anthony
 *   APPLICANT: Johnson, Kevin
 *   APPLICANT: Hoogenboom, Henricus
 *   APPLICANT: Griffiths, Andrew
 *   APPLICANT: Jackson, Ronald
 *   APPLICANT: Holliger, Kasper
 *   APPLICANT: Marks, James
 *   APPLICANT: Clackson, Timothy
 *   APPLICANT: Chiswell, David
 *   APPLICANT: Winter, Gregory
 *   APPLICANT: Bonest, Timothy
 * TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
 * FILE REFERENCE: 213839-0004
 * CURRENT APPLICATION NUMBER: US/09/196,522
 * CURRENT FILING DATE: 1998-11-28
 * PRIOR APPLICATION NUMBER: GB 9015198.6
 * PRIOR FILING DATE: 1990-07-10
 * PRIOR APPLICATION NUMBER: GB 9022845.3
 * PRIOR FILING DATE: 1990-10-19
 * PRIOR APPLICATION NUMBER: GB 9022845.3
 * PRIOR FILING DATE: 1990-10-19
 * PRIOR APPLICATION NUMBER: GB 9024503.6
 * PRIOR FILING DATE: 1990-11-12
 * PRIOR APPLICATION NUMBER: GB 9104744.9
 * PRIOR FILING DATE: 1991-03-06
 * PRIOR APPLICATION NUMBER: GB 9110549.4
 * PRIOR FILING DATE: 1991-05-15
 * PRIOR APPLICATION NUMBER: PCT/GB94/01134
 * PRIOR FILING DATE: 1991-07-10
 * PRIOR APPLICATION NUMBER: US 07/971,857
 * PRIOR FILING DATE: 1993-01-08
 * PRIOR APPLICATION NUMBER: US 08/484,893
 * PRIOR FILING DATE: 1995-06-07
 * NUMBER OF SEQ ID NOS: 272
 * SOFTWARE: PatentIn version 3.1
 * SEQ ID NO: 171
 * LENGTH: 111
 * TYPE: PRT
 * ORGANISM: Homo sapiens
 * US-09-196,522-171

Query Match          92.4%; Score 85; DB 2; Length 111;
Best Local Similarity 94.1%; Prd. No. 3.1e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 IIYPGDSDTIYSPSFQG 17
Db      50 IIYPGDSDTRISPSFQG 66

RESULT 8
US-08-545-809A-133
  Sequence 133; Application US/08545809A
  Patent No. 6916605
  GENERAL INFORMATION:
    APPLICANT: Horjo, Tasuku
    APPLICANT: Matsuda, Fumihiko
    TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
    TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
    NUMBER OF SEQUENCES: 145
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Fish & Richardson, P.C.
      STREET: 225 Franklin Street
      CITY: Boston
      STATE: MA
      COUNTRY: US
      ZIP: 02110-2804

```

TELEX: 200154
 INFORMATION FOR SEQ ID NO: 133:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 117 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 133:
 us-09-515-697-133

Query Match 92.4%; Score 85; DB 2; Length 117;
 Best Local Similarity 94.1%; Pred. No. 3.3e-05;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGDDDTIYSPSFQG 17
 Db 69 IYPGDSSTRISPSFQG 85

RESULT 10
 US-09-025-769B-26
 Sequence 26, Application US/09025769B
 GENERAL INFORMATION:
 APPLICANT: Knapik, Achim
 APPLICANT: Pack, Peter
 APPLICANT: Ilag, Vic
 APPLICANT: Ge, Liming
 APPLICANT: Moroney, Simon
 APPLICANT: Plueckthun, Andreas
 TITLE OF INVENTION: Protein/ (Poly) peptide libraries
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 ZIP: 10021
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/490-070A
 FILING DATE: 24-Jan-2000
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Colin G. Sandercock, Esq.
 REFERENCE/DOCKET NUMBER: 31_298
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 912-2000
 TELEFAX: (202) 912-2020
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 US-09-490-070A-26

RESULT 11
 US-09-490-070A-26
 / Sequence 26, Application US/09490070A
 / Patent No. 6696248
 / GENERAL INFORMATION:
 / APPLICANT: Knappik, Achim
 / APPLICANT: Pack, Peter
 / APPLICANT: Ilag, Vic
 / APPLICANT: Ge, Liming
 / APPLICANT: Moroney, Simon
 / APPLICANT: Plueckthun, Andreas
 / TITLE OF INVENTION: Protein/ (Poly) peptide libraries
 / NUMBER OF SEQUENCES: 373
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
 / White & McAuliffe
 / STREET: 1666 K Street, N.W., Suite 300
 / CITY: Washington
 / STATE: D.C.
 / COUNTRY: USA
 / ZIP: 20006
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/490-070A
 FILING DATE: 24-Jan-2000
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Colin G. Sandercock, Esq.
 REGISTRATION NUMBER: 31_298
 REFERENCE/DOCKET NUMBER: 37629-0005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 912-2000
 TELEFAX: (202) 912-2020
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 US-09-490-070A-26

Query Match 92.4%; Score 85; DB 2; Length 119;
 Best Local Similarity 94.1%; Pred. No. 3.3e-05;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGDSDTIYSPSFQG 17
 Db 50 IYPGDSSTRYSPSFQG 66

RESULT 12
 US-09-490-153-26
 / Sequence 26, Application US/09490153
 / Patent No. 6706484
 / GENERAL INFORMATION:
 / APPLICANT: Knappik, Achim
 / APPLICANT: Pack, Peter
 / APPLICANT: Ilag, Vic
 / APPLICANT: Ge, Liming
 / APPLICANT: Moroney, Simon
 / APPLICANT: Plueckthun, Andreas
 / TITLE OF INVENTION: Protein/ (Poly) peptide libraries
 / NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/490,153
 FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,769B
 FILING DATE: 18-FEB-1998
 APPLICATION NUMBER: EP 95 11 3021.0

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)596-9000
 TELEX/FAX: (212)596-9090

ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: MORPHO/5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)596-9000
 TELEX/FAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 US-09-490-324-26

RESULT 14
 US-09-025-769B-40
 / Sequence 40, Application US/09025769B
 / Patient No. 6300064

GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 APPLICANT: Pack, Peter
 APPLICANT: Ilag, Vic
 APPLICANT: Ge, Liming
 APPLICANT: Moroney, Simon
 APPLICANT: Pueckthun, Andreas
 TITLE OF INVENTION: Protein/(Poly)peptide libraries
 NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,769B
 FILING DATE: 18-FEB-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: MORPHO/5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)596-9000
 TELEX/FAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 40:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acids

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; TYPE: amino acid
; STRANDEDNESS:
; MOLECULE TYPE: protein
; US-09-025-769B-40

Query Match      92.4%;  Score 85;  DB 2; Length 120;
Best Local Similarity 94.1%;  Pred. No. 3.4e-05;
Matches 16;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy      1  I I Y P G D S D T I Y S P S F Q G 17
          ||||| | | | | | | | | | |
Db      50  I I Y P G D S D T R Y S P S F Q G 66

RESULT 15
US-09-025-769B-67
Sequence 67, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Illeg, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-8090
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-67

Query Match      92.4%;  Score 85;  DB 2; Length 120;
Best Local Similarity 94.1%;  Pred. No. 3.4e-05;
Matches 16;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy      1  I I Y P G D S D T I Y S P S F Q G 17
          ||||| | | | | | | | | | |
Db      50  I I Y P G D S D T R Y S P S F Q G 66

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Result No.	Score	Query	Match	Length	DB ID	Description
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1	92	100.0	17	5	US_10-769-144-14	Sequence 14, APP1
2	92	100.0	17	5	US_10-503-191-14	Sequence 14, APP1
3	92	100.0	116	3	US_09-851-614-4	Sequence 4, APP1
4	92	100.0	116	4	US_10-035-637-4	Sequence 4, APP1
5	92	100.0	116	5	US_10-769-144-2	Sequence 4, APP1
6	92	100.0	116	5	US_10-903-191-4	Sequence 4, APP1
7	92	100.0	411	5	US_10-769-144-12	Sequence 12, APP1
8	92	100.0	411	5	US_10-503-191-12	Sequence 12, APP1
9	92	100.0	468	5	US_10-769-144-2	Sequence 2, APP1
10	92	100.0	468	5	US_10-903-191-2	Sequence 2, APP1
11	92	100.0	613	5	US_10-769-144-10	Sequence 10, APP1
12	92	100.0	613	5	US_10-503-191-10	Sequence 10, APP1
13	85	92.4	17	4	US_10-384-060-40	Sequence 40, APP1
14	85	92.4	17	4	US_10-574-932-6	Sequence 6, APP1
15	85	92.4	17	4	US_10-179-741-6	Sequence 6, APP1
16	85	92.4	17	4	US_10-125-520-369	Sequence 369, APP1
17	85	92.4	17	5	US_10-684-957-35	Sequence 35, APP1
18	85	92.4	17	5	US_10-538-265-95	Sequence 95, APP1
19	85	92.4	17	5	US_10-722-332-55	Sequence 55, APP1
20	85	92.4	17	5	US_10-726-332-73	Sequence 73, APP1
21	85	92.4	17	5	US_10-126-332-88	Sequence 88, APP1
22	85	92.4	17	5	US_10-723-332-91	Sequence 91, APP1
23	85	92.4	17	5	US_10-851-658-93	Sequence 93, APP1
24	85	92.4	17	5	US_10-382-725-6	Sequence 6, APP1
25	85	92.4	82	4	US_10-078-955-5	Sequence 5, APP1
26	85	92.4	98	3	US_09-850-165-89	Sequence 89, APP1
27	85	92.4	98	4	US_10-194-975-45	Sequence 45, APP1

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; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-035-637-4

Query Match 100.0%; Score 92; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-903-191-14

QY 1 IIYPGDSDTIYSPSFQG 17
Db 50 IIYPGDSDTIYSPSFQG 66

RESULT 5
US-10-769-144-4
; Sequence 4, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION
; APPLICANT: Keler, Tibor
; ENDRES, Michael
; APPLICANT: He, Lizen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-769-144-4

Query Match 100.0%; Score 92; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-903-191-14

QY 1 IIYPGDSDTIYSPSFQG 17
Db 50 IIYPGDSDTIYSPSFQG 17

RESULT 6
US-10-903-191-4
; Sequence 4, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION
; APPLICANT: Keler, Tibor
; ENDRES, Michael
; APPLICANT: He, Lizen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-903-191-4

Query Match 100.0%; Score 92; DB 3; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-903-191-4

QY 1 IIYPGDSDTIYSPSFQG 17
Db 50 IIYPGDSDTIYSPSFQG 66

RESULT 6
US-10-035-637-4
; Sequence 4, Application US/10035637
; Publication No. US2003031667A1
; GENERAL INFORMATION
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: MXI-166CP
; CURRENT APPLICATION NUMBER: US/10/035,637
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-903-191-4

Query Match 100.0%; Score 92; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Best Local Similarity 100.0%; Pred. No. 1.3e-06; Mismatches 0; Indels 0; Gaps 0; Query 1 IIYPGDSDTIYSPSPFG 17 Database 50 IIYPGDSDTIYSPSPFG 66 Result 9 US-10-769-144-2 Sequence 2, Application US/10769144 Publication No. US2004024815A1 General Information: ; GENERAL INFORMATION: ; ; APPLICANT: Keller, Tibor ; APPLICANT: Endres, Michael ; APPLICANT: He, Lizhen ; APPLICANT: Ramakrishna, Venky ; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES ; TITLE OF INVENTION: THEREFOR ; FILE REFERENCE: MXI-301 ; CURRENT APPLICATION NUMBER: US/10/769,144 ; CURRENT FILING DATE: 2004-01-30 ; PRIORITY APPLICATION NUMBER: 60/443979 ; PRIOR FILING DATE: 2003-01-31 ; NUMBER OF SEQ ID NOS: 32 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO: 12 LENGTH: 411 TYPE: PRT ORGANISM: Homo sapiens US-10-769-144-12

Query Match 100.0%; Score 92; DB 5; Length 411; Best Local Similarity 100.0%; Pred. No. 5.4e-06; Mismatches 0; Indels 0; Gaps 0; Query 1 IIYPGDSDTIYSPSPFG 17 Database 191 IIYPGDSDTIYSPSPFG 207 Result 10 US-10-903-191-2 Sequence 2, Application US/10903191 Publication No. US20050180983A1 General Information: ; GENERAL INFORMATION: ; ; APPLICANT: Keller, Tibor ; APPLICANT: Endres, Michael ; APPLICANT: He, Lizhen ; APPLICANT: Ramakrishna, Venky ; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES ; TITLE OF INVENTION: THEREFOR ; FILE REFERENCE: MXI-301CP ; CURRENT APPLICATION NUMBER: US/10/903,191 ; CURRENT FILING DATE: 2004-07-30 ; PRIORITY APPLICATION NUMBER: 60/443979 ; PRIOR FILING DATE: 2003-01-31 ; NUMBER OF SEQ ID NOS: 32 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO: 2 LENGTH: 468 TYPE: PRT ORGANISM: Homo sapiens US-10-903-191-2

Query Match 100.0%; Score 92; DB 5; Length 468; Best Local Similarity 100.0%; Pred. No. 6.2e-06; Mismatches 0; Indels 0; Gaps 0; Query 1 IIYPGDSDTIYSPSPFG 17 Database 69 IIYPGDSDTIYSPSPFG 85 Result 11 US-10-769-144-10

Sequence 10, Application US/10769144
 Publication No. US20040248215A1
 GENERAL INFORMATION:
 APPLICANT: Keler, Tibor
 APPLICANT: Endres, Michael
 APPLICANT: He, Lizhen
 APPLICANT: Ramakrishna, Venky
 TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
 FILE REFERENCE: MXI-301
 CURRENT APPLICATION NUMBER: US/10/769,144
 CURRENT FILING DATE: 2004-01-10
 PRIOR APPLICATION NUMBER: 60/443979
 PRIOR FILING DATE: 2003-01-31
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 10
 LENGTH: 613
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-769-144-10

Query Match 100.0%; Score 92; DB 5; Length 613;
 Best Local Similarity 100.0%; Pred. No. 8.4e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 IIYPGDSDTIYSPSPFG 17
 Db 69 IIYPGDSDTIYSPSPFG 85

RESULT 12
 US-10-903-191-10
 Sequence 10, Application US/10903191
 Publication No. US20050180983A1
 GENERAL INFORMATION:
 APPLICANT: Keler, Tibor
 APPLICANT: Endres, Michael
 APPLICANT: He, Lizhen
 APPLICANT: Ramakrishna, Venky
 TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
 FILE REFERENCE: MXI-201CP
 CURRENT APPLICATION NUMBER: US/10/903,191
 CURRENT FILING DATE: 2004-07-30
 PRIOR APPLICATION NUMBER: 10/769144
 PRIOR FILING DATE: 2004-01-30
 PRIOR APPLICATION NUMBER: 60/443979
 PRIOR FILING DATE: 2003-01-31
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 10
 LENGTH: 613
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-903-191-10

Query Match 100.0%; Score 92; DB 5; Length 613;
 Best Local Similarity 100.0%; Pred. No. 8.4e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 IIYPGDSDTIYSPSPFG 17
 Db 69 IIYPGDSDTIYSPSPFG 85

RESULT 13
 US-10-384-06-40
 Sequence 40, Application US/10384060
 Publication No. US20030226155A1
 GENERAL INFORMATION:
 APPLICANT: SADEGH, Homayoun
 APPLICANT: PRIOR, Christopher P.

APPLICANT: TURNER, Andrew
 TITLE OF INVENTION: MODIFIED TRANSPIRIN-ANTIBODY FUSION PROTEINS
 FILE REFERENCE: 547105004.US
 CURRENT APPLICATION NUMBER: US/10/384,060
 CURRENT FILING DATE: 2003-03-10
 PRIOR APPLICATION NUMBER: US 10/231,494
 PRIOR FILING DATE: 2002-08-30
 PRIOR APPLICATION NUMBER: US 60/334,059
 PRIOR FILING DATE: 2001-11-30
 PRIOR APPLICATION NUMBER: US 60/315,745
 PRIOR FILING DATE: 2001-08-30
 PRIOR APPLICATION NUMBER: US 60/405,977
 PRIOR FILING DATE: 2002-08-30
 NUMBER OF SEQ ID NOS: 80
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 40
 LENGTH: 17
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: VH CDR2 sequence
 US-10-384-06-40

RESULT 14
 US-10-374-932-6
 Sequence 6, Application US/10374932
 Publication No. US2003023586A1
 GENERAL INFORMATION:
 APPLICANT: van de Winkel, Jan G.J.
 APPLICANT: van Dijk, Marcus Antonius
 APPLICANT: Schuurman, Janine
 APPLICANT: Gerritsen, Arrouit F.
 APPLICANT: Baadsgaard, Ole
 APPLICANT: Petersen, Jorgen
 TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)
 FILE REFERENCE: GM1-02ACP
 CURRENT APPLICATION NUMBER: US/10/374,932
 CURRENT FILING DATE: 2003-02-26
 PRIOR APPLICATION NUMBER: US 60/314,731
 PRIOR FILING DATE: 2001-08-23
 PRIOR APPLICATION NUMBER: US 10/226615
 PRIOR FILING DATE: 2002-08-23
 NUMBER OF SEQ ID NOS: 31
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 6
 LENGTH: 17
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-374-932-6

RESULT 15
 US-10-379-741-6
 Sequence 6, Application US/10379741
 Publication No. US20040071702A1
 GENERAL INFORMATION:

```
; APPLICANT: van de Winkel, Jan G.J.  
; APPLICANT: van Dijk, Marcus Antonius  
; APPLICANT: Schuurman, Janine F.  
; APPLICANT: Gerritsen, Arnout F.  
; APPLICANT: Baadgaard, Ole  
; APPLICANT: Petersen, Jorgen  
TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)  
FILE REFERENCE: GMI-024CP2  
CURRENT APPLICATION NUMBER: US/10/379,741  
CURRENT FILING DATE: 2003-03-05  
PRIOR APPLICATION NUMBER: US 60/314,731  
PRIOR FILING DATE: 2001-08-23  
PRIOR APPLICATION NUMBER: US 10/226615  
PRIOR FILING DATE: 2002-08-23  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-379-741-6  
Query Match 92.4%; Score 85; DB 4; Length 17;  
Best Local Similarity 94.1%; Pred. No. 2e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy ||||| ||||| |||||  
Db 1 IIYPGDSITYSPSFQG 17  
1 IIYPGDSITYSPSFQG 17
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Search completed: December 3, 2005, 14:17:35
Job time : 24.3143 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2005, 13:48:29 ; Search time 0.971429 Seconds
(without alignments)
83.796 Million cell updates/sec

Title: US-10-769-144-14
Perfect score: 92
Sequence: 1 ILYPGDSDTIYSPSFQG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	85	92.4	98	7	US-11-054-669-45	Sequence 45, App1
2	85	92.4	98	7	US-11-054-554-56	Sequence 56, App1
3	85	92.4	252	7	US-11-054-515-1537	Sequence 1537, App1
4	81	88.0	248	7	US-11-054-515-1995	Sequence 1995, App1
5	80	87.0	249	7	US-11-054-515-1312	Sequence 1312, App1
6	77	83.7	248	7	US-11-054-515-1	Sequence 1, App1
7	69	75.0	249	7	US-11-054-515-1957	Sequence 1957, App1
8	61	66.3	119	7	US-11-054-661-124	Sequence 124, App1
9	58	63.0	248	6	US-10-512-184-36	Sequence 36, App1
10	58	63.0	615	6	US-10-512-184-50	Sequence 50, App1
11	57	62.0	17	6	US-10-512-185-27	Sequence 27, App1
12	57	62.0	121	6	US-10-502-145-21	Sequence 21, App1
13	57	62.0	247	7	US-11-084-717-21	Sequence 21, App1
14	57	62.0	543	6	US-10-495-664-3	Sequence 3, App1
15	56	60.9	248	7	US-11-054-515-2088	Sequence 2088, App1
16	55	59.8	251	7	US-11-054-515-1390	Sequence 1390, App1
17	54	58.7	247	7	US-11-084-717-23	Sequence 23, App1
18	54	58.7	247	7	US-11-084-717-25	Sequence 25, App1
19	53	57.6	247	7	US-11-054-515-2103	Sequence 2103, App1
20	51	55.4	249	7	US-11-054-515-1970	Sequence 1970, App1
21	48	52.2	17	6	US-10-839-799-116	Sequence 116, App1
22	48	52.2	98	7	US-11-054-669-11	Sequence 11, App1
23	48	52.2	117	6	US-10-839-799-132	Sequence 132, App1
24	48	52.2	125	7	US-11-056-074-58	Sequence 58, App1
25	48	52.2	136	6	US-10-839-799-29	Sequence 29, App1

ALIGNMENTS

RESULT 1
US-11-054-669-45
; Sequence 45, Application US/1104669
; Publication No. US2005261180A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/034,669
; PRIORITY FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIORITY FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIORITY FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-054-669-45

Query Match 92.4%; Score 85; DB 7; Length 98;
Best Local Similarity 94.1%; Pred. No. 9.8e-08;
Matchers 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ILYPGDSDTIYSPSFQG 17
Db 50 ILYPGDSDTRYSPSFQG 66

RESULT 2
US-11-084-554-56
; Sequence 56, Application US/11084554
; Publication No. US2005260579A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Srid-Ai
; APPLICANT: Kellermann, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: ABGENIX 100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24

NUMBER OF SEQ ID NOS: 266
SEQ ID NO: 56
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-11-08-554-56

Query Match 92.4%; Score 85; DB 7; Length 98;
 Best Local Similarity 94.1%; Pred. No. 9.8e-08;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTIYSPSPQG 17
 Db 50 IIYPGDSDTIYSPSPFQG 66

RESULT 3
US-11-054-515-1537
Sequence 1537. Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
FILE REFERENCE: PF52P3
CURRENT APPLICATION NUMBER: US/11/054,515
PRIOR FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-05-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/311,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO: 1995
LENGTH: 248
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1995

Query Match 88.0%; Score 81; DB 7; Length 248;
 Best Local Similarity 83.2%; Pred. No. 1.2e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTIYSPSPQG 17
 Db 50 IIYPGDSDTIYSPSPQG 66

RESULT 5
US-11-054-515-1312
Sequence 1312. Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF52P3
CURRENT APPLICATION NUMBER: US/11/054,515
PRIOR FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/311,469
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO: 1537
LENGTH: 252
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1537

Query Match 92.4%; Score 85; DB 7; Length 252;
 Best Local Similarity 94.1%; Pred. No. 2.6e-07;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTIYSPSPQG 17
 Db 50 IIYPGDSDTIYSPSPQG 66

RESULT 4
US-11-054-515-1995
Sequence 1995. Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
FILE REFERENCE: PF52P3
CURRENT APPLICATION NUMBER: US/11/054,515
PRIOR FILING DATE: 2005-02-16
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO: 1312
LENGTH: 249
TYPE: PRT

; ORGANISM: Homo sapiens
 US-11-054-515-1312
 Query Match 87.0%; Score 80; DB 7; Length 249;
 Best Local Similarity 88.2%; Pred. No. 1.7e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 SEQ ID NO: 1 IYPGDSDTIYSPSFGQ 17
 Db 50 IYPGDSNTRYSPSFGQ 66

RESULT 6
 Sequence 1, Application US/11054515
 Publication No. US20050255532A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 CURRENT APPLICATION NUMBER: US/11/054,515
 CURRENT FILING DATE: 2005-02-10
 PRIOR APPLICATION NUMBER: 60/543,296
 PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: 60/580,347
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 10/293,418
 PRIOR FILING DATE: 2002-11-14
 PRIOR APPLICATION NUMBER: 60/331,469
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/340,817
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 09/880,748
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: 60/293,499
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/277,379
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/276,248
 PRIOR FILING DATE: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/240,816
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 3247
 SEQ ID NO: 1
 LENGTH: 248
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-054-515-1
 Query Match 83.7%; Score 77; DB 7; Length 248;
 Best Local Similarity 82.4%; Pred. No. 5.2e-06;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 SEQ ID NO: 1 IYPGDSDTIYSPSFGQ 17
 Db 50 IYPGDSNTRYSPSFGQ 66

RESULT 7
 US-11-054-515-1957
 Sequence 1957, Application US/11054515
 Publication No. US20050255532A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 FILE REFERENCE: PP23P3
 CURRENT APPLICATION NUMBER: US/11/054,515
 CURRENT FILING DATE: 2005-02-10
 PRIOR APPLICATION NUMBER: 60/543,296
 PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: 60/580,347
 PRIOR FILING DATE: 2004-06-18

RESULT 8
 US-11-054-669-124
 Sequence 124, Application US/11054669
 Publication No. US20050261480A1
 GENERAL INFORMATION:
 APPLICANT: Foote, Jefferson
 TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
 FILE REFERENCE: 30219/US/3
 CURRENT APPLICATION NUMBER: US/11/054,669
 CURRENT FILING DATE: 2005-02-08
 PRIOR APPLICATION NUMBER: US 10/194,975
 PRIOR FILING DATE: 2002-07-12
 PRIOR APPLICATION NUMBER: US 60/305,111
 PRIOR FILING DATE: 2001-07-12
 NUMBER OF SEQ ID NOS: 124
 SOFTWARE: Patentin version 3.3
 SEQ ID NO: 124
 LENGTH: 119
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-054-669-124
 Query Match 66.3%; Score 61; DB 7; Length 119;
 Best Local Similarity 68.4%; Pred. No. 0.00066;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

RESULT 9
 US-10-512-184-36
 Sequence 36, Application US/10512184
 Publication No. US20050244901A1
 GENERAL INFORMATION:
 APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e. V.
 TITLE OF INVENTION: Antibodies, recombinant antibodies, antibody fragments and fusions mediated plant disease resistance against fungi

```

FILE REFERENCE: 3581_01US01 ; TYPE: PRT
CURRENT APPLICATION NUMBER: US/10/512,184 ; ORGANISM: Mus musculus
CURRENT FILING DATE: 2004-10-22 ; SEQ ID NO: 72 ; US-10-502-145-27
NUMBER OF SEQ ID NOS: 72 ; SOFTWARE: PatentIn Ver. 2.1 ; Query Match Score: 57; DB 6; Length 17;
SEQ ID NO: 36 ; LENGTH: 248 ; Matches: 10; Conservative: 3; Mismatches: 3; Indels: 0; Gaps: 0;
TYPE: PRT ; ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: scFv SS2 with
OTHER INFORMATION: specificity against Sclerocinia sclerotiorum;
OTHER INFORMATION: originates from Mus musculus.
US-10-512-184-36

RESULT 12
US-10-502-145-21 ; Query Match Score: 57; DB 6; Length 17;
Best Local Similarity: 62.5%; Pred. No. 0.0056; ; SEQ ID NO: 21 ; Publication US/10502145
Matches: 10; Conservative: 3; Mismatches: 3; Indels: 0; Gaps: 0;
GENERAL INFORMATION: ; Publication No. US2005024406A1
APPLICANT: MACKAY, CHARLES REAY ; TITLE OF INVENTION: Anti-C5aR antibodies and uses thereof
FILE REFERENCE: RICE-032 ; CURRENT APPLICATION NUMBER: US/10/502,145
TITLE OF INVENTION: Anti-C5aR antibodies and uses thereof ; PRIORITY APPLICATION NUMBER: US/10/502,145
FILE REFERENCE: RICE-032 ; CURRENT FILING DATE: 2004-07-19
PRIORITY APPLICATION NUMBER: US/10/502,145 ; PRIORITY FILING DATE: 2002-01-25
PRIORITY FILING DATE: 2002-01-25 ; NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1 ; SEQ ID NO: 21
LENGTH: 121 ; TYPE: PRT
ORGANISM: Mus musculus ; US-10-502-145-21

Query Match Score: 57; DB 6; Length 121;
Best Local Similarity: 62.5%; Pred. No. 0.0044; ; SEQ ID NO: 17 ; Publication US/10502145
Matches: 10; Conservative: 3; Mismatches: 4; Indels: 0; Gaps: 0;
GENERAL INFORMATION: ; Publication No. US2005024406A1
APPLICANT: MACKAY, CHARLES REAY ; TITLE OF INVENTION: Anti-C5aR antibodies and uses thereof
FILE REFERENCE: RICE-032 ; CURRENT APPLICATION NUMBER: US/10/502,145
PRIORITY APPLICATION NUMBER: US/10/502,145 ; PRIORITY FILING DATE: 2002-01-25
PRIORITY FILING DATE: 2002-01-25 ; NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1 ; SEQ ID NO: 21
LENGTH: 121 ; TYPE: PRT
ORGANISM: Mus musculus ; US-10-502-145-21

RESULT 13
US-11-084-717-21 ; Query Match Score: 57; DB 6; Length 121;
Best Local Similarity: 62.5%; Pred. No. 0.0044; ; SEQ ID NO: 17 ; Publication US/11084717
Matches: 10; Conservative: 3; Mismatches: 4; Indels: 0; Gaps: 0;
GENERAL INFORMATION: ; Publication No. US20050260136A1
APPLICANT: GEORGIOTOU, GEORGE ; TITLE OF INVENTION: SELECTION OF BACTERIAL INNER-MEMBRANE ANCHOR POLYPEPTIDES
FILE REFERENCE: UTSB-723US ; CURRENT APPLICATION NUMBER: US/11/084,717
APPLICANT: JEONG, KI-JUN ; CURRENT FILING DATE: 2005-03-18
APPLICANT: HARVEY, BARRETT R. ; PRIORITY APPLICATION NUMBER: 60/554,324
APPLICANT: IVERSON, BRENT L. ; PRIORITY FILING DATE: 2004-03-18
APPLICANT: HARVEY, BARRETT R. ; LENGTH: 247
APPLICANT: IVERSON, BRENT L. ; PRIORITY APPLICATION NUMBER: 10/620,278
APPLICANT: IVERSON, BRENT L. ; PRIORITY FILING DATE: 2003-07-15
APPLICANT: MACKAY, CHARLES REAY ; TYPE: PRT
APPLICANT: MACKAY, CHARLES REAY ; ORGANISM: Artificial Sequence
APPLICANT: MACKAY, CHARLES REAY ; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
APPLICANT: MACKAY, CHARLES REAY ; OTHER INFORMATION: Peptide
APPLICANT: MACKAY, CHARLES REAY ; US-11-084-717-21
APPLICANT: MACKAY, CHARLES REAY ; NUMBER OF SEQ ID NOS: 34
APPLICANT: MACKAY, CHARLES REAY ; SEQ ID NO: 27
APPLICANT: MACKAY, CHARLES REAY ; LENGTH: 17
APPLICANT: MACKAY, CHARLES REAY ; SEQ ID NO: 27
APPLICANT: MACKAY, CHARLES REAY ; LENGTH: 247;
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Best Local Similarity 62.5%; Pred. No. 0.0092; 4; Indels 0; Gaps 0;
 Matches 10; Conservative 2; Mismatches 4;
 SEQ ID NO: 2088
 LENGTH: 248
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-054-515-2088

RESULT 14
 US-10-495-664-3
 Sequence 3, Application US/10495664
 Publication No. US/050244416A1
 GENERAL INFORMATION:
 TITLE OF INVENTION: BISPECIFIC ANTI-CD28 ANTIBODY MOLECULE
 FILE REFERENCE: 034258-0801
 CURRENT APPLICATION NUMBER: US/10/495,664
 CURRENT FILING DATE: 2004-05-12
 PRIOR APPLICATION NUMBER: PCT/EP02/12545
 PRIOR FILING DATE: 2002-11-09
 PRIOR APPLICATION NUMBER: DE 101 56 482.1
 PRIOR FILING DATE: 2001-11-12
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: Patentin Ver. 3.3
 SEQ ID NO 3
 LENGTH: 543
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: protein construct
 US-10-495-664-3

Query Match 60.9%; Score 56; DB 7; Length 248;
 Best Local Similarity 75.0%;
 Matches 12; Conservative 0; Mismatches 4;
 Indels 0; Gaps 0;

Qy 2 IYPGDSDTIYSPSFG 17
 Db 51 IDPDSYTNYSPSRG 66

Search completed: December 3, 2005, 14:17:55
 Job time : 1.97143 secs

RESULT 15
 US-11-054-515-2088
 Sequence 2088, Application US/11054515
 Publication No. US/050255532A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
 FILE REFERENCE: P523P3
 CURRENT APPLICATION NUMBER: US/11/054,515
 CURRENT FILING DATE: 2005-02-10
 PRIOR APPLICATION NUMBER: 60/543,296
 PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: 60/580,347
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 10/293,418
 PRIOR FILING DATE: 2002-11-14
 PRIOR APPLICATION NUMBER: 60/331,469
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/340,817
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 09/880,748
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: 60/293,499
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/277,379
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/276,248
 PRIOR FILING DATE: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/240,816
 PRIOR FILING DATE: 2000-10-17

Remaining Prior Application data removed - See File Wrapper or PALM.

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	Gapext 0.5	
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Adp47219 Human pho	ADP47219	
Aae31207 Human AB-	AAE31207	
Aea16229 Anti-huma	AEA16229	
Aab61621 Human leu	AB61621	
Adl10771 Anti-TNFA	ADL10771	
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Abro1545 Human ant	ABR01545	
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Adp47114 Human pho	ADP47114	
Adp47092 Human pho	ADP47092	
Adp47224 Human pho	ADP47224	
Adz42024 Ig H chai	ADZ42024	
Adp47228 Human ant	ADP47228	
Adp2260 Human ant	ADP2260	
Adp22194 Human ant	ADP22194	
Adk18899 Anti-huma	ADK18899	
Adk18899 Anti-huma	ADK18899	
Adp10527 Human ant	ADP10527	

ALIGNMENT S

monoclonal antibody B11 variable heavy chain protein.
B11; antigen binding portion; dendritic cell; receptor; growth; cytolysis; pathogen; virus; bacterium; immune disease; inflammatory disorder; rheumatoid arthritis; scleritis; diabetes mellitus; immunomodulatory; inflammatory; antiarthritic; immunoprotective; antianemic; endocrine; dermatological; antithyroid; ophthalmological; muscular.

卷之三

Human monoclonal antibody B11 variable heavy chain protein.
Human; monoclonal antibody; B11; antigen binding porion; dendritic cell; mannose receptor; growth; cytolytic; pathogen; virus; bacterium; autoimmune disease; inflammatory disorder; rheumatoid arthritis; multiple sclerosis; diabetes mellitus; immunomodulatory; antiinflammatory; antirheumatic; antiarthritic; neuroprotective; antidiabetic; antinaemic; endocrine; dermatological; antithyroid; ophthalmological; muscular; uropathic.

No. is the number of results predicted by chance to have a greater score than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	621	100.0	116	5 AAM48005	Aam48005 Human mon
2	621	100.0	116	8 ADR48821	Adr46821 Human ant
3	621	100.0	411	8 ADR48829	Adr46829 Human pB1
4	621	100.0	468	8 ADR48819	Adr46819 Human ant
5	621	100.0	613	8 ADR48827	Adr46827 Human bet
6	560	90.2	117	8 ADP47223	Adp47223 Human pho
7	558.5	89.9	245	4 AAB61622	Aab61622 Human leu
8	558	89.9	117	8 ADP47094	Adp47094 Human pho
9	556	89.5	120	2 AAW21555	Aaw21555 Human Ab
10	556	89.5	120	6 ABJ11677	Abj11677 Ant body
11	556	89.5	120	6 ABJ11720	Abj118720 Ant body
12	552.5	89.0	252	5 ABP45226	Abp45226 Human Bly
13	552.5	89.0	252	7 ADG93353	Adg93353 Single ch
14	552.5	89.0	266	8 ADP68905	Adp68905 Human lun
15	552	88.9	117	8 ADP47229	Adp47229 Human pho
16	550.5	88.6	118	8 ADP47230	Adp47230 Human pho
17	550	88.6	224	6 ABR01533	Abr01533 Human ant
18	550	88.6	224	6 ABR01530	Abr01530 Human ant
19	550	88.6	226	6 ABR01522	Abr01522 Human ant
20	549.5	88.5	474	9 AEAI1652	Aea11652 Heavy cha
21	549.5	88.5	474	9 AEAI1653	Aea11653 Heavy cha
22	549.5	88.5	474	9 AEAI18909	Aea118909 Variant h
23	549.5	88.5	474	9 AEAI1908	Aea11908 Heavy cha
24	549.5	88.5	474	9 AEAI18548	Aea118548 Heavy cha

omo sapiens.

WO2001185798-A2.
15-NOV-2001.
08-MAY-2000; 2001WO-US015114.
08-MAY-2000; 2000US-0203126P.
07-SEP-2000; 2000US-0230739P.
(MEDA-) MEDAREX INC.
Deo YM, Keller T;
WPI: 2002-089788/12.
N-PSDB; ARA05500.
New human monoclonal antibodies specific for dendritic cells, useful for inhibiting growth or inducing cytolysis of a dendritic cell and treating or preventing a dendritic cell mediated disease, e.g., autoimmune disorders.

Example 2; Fig 13; 95pp; English.

The invention relates to human monoclonal antibodies or their antigen binding portions that specifically bind to dendritic cells and has one or more of the following characteristics: (a) a binding affinity constant to a dendritic cell of at least about 10 to the power 7 M-1; (b) the ability

CC to opsonise a dendritic cell; (c) the ability to internalise after binding to dendritic cells; or (d) the ability to activate dendritic cells. The isolated human monoclonal antibody or its antigen-binding portion may also have any of the following characteristics: (a) mediates cytolysis of dendritic cells in the presence of human effector cells; or (b) inhibits growth of dendritic cells. The antibodies or its antigen binding portion, binds to and blocks the human mannose receptor on dendritic cells. The antibodies have immunomodulatory, antiinflammatory, antirheumatic, neuroprotective, antidiabetic, antianemic, endocrine, dermatological, antithyroid, uropathic, ophthalmological and muscular activity. The antibodies or their antigen-binding fragments are useful for inhibiting growth of a dendritic cell, inducing cytolysis of a dendritic cell, treating or preventing a dendritic cell mediated disease, detecting the presence of a dendritic cell, targeting an antigen to a dendritic cell and preventing binding of a pathogen (a virus or a bacterium) to human mannose receptor on dendritic cells. In particular, the antibodies may be used to treat, autoimmune disease, graft versus host disease, immune system or inflammatory disorders (e.g. rheumatoid arthritis), multiple sclerosis, diabetes mellitus, myasthenia gravis, pernicious anaemia, Addison's disease, lupus erythematosus, Reiter's syndrome and Graves disease. The present sequence is that of the human monoclonal antibody B11 variable heavy chain, useful to the invention

XX Sequence 116 AA;

Query Match Score 621; DB 5; Length 116;
 Best Local Similarity 100.0%; Pred. No. 7.2e-50;
 Matches 116; Conservative 0; Indels 0; Gaps 0;
 Matches 116; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRLSCKGSQDSFTTYIGWVRQMPGKGLEWMMGIYPGDSDTIY 60
 Db 1 EVQLVQSGAEVKKPGESLRLSCKGSQDSFTTYIGWVRQMPGKGLEWMMGIYPGDSDTIY 60

Qy 61 SPSFQQVTISADKSISTAYLQWSSLKLASDTSAMYCTRDGVYDYGQTLVTVSS 116
 Db 61 SPSFQQVTISADKSISTAYLQWSSLKLASDTSAMYCTRDGVYDYGQTLVTVSS 116

RESULT 2
 ADR46821
 ID ADR46821 standard; protein; 116 AA.
 XX
 AC ADR46821;
 DT 18-NOV-2004 (first entry)
 XX Human antibody B11 heavy chain variable region protein SEQ ID NO:4.
 XX molecular conjugate; monoclonal antibody; human antigen presenting cell;
 KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
 KW betahCG; beta chorionic gonadotropin; antibody; human chorionic gonadotropin;
 KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
 KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimarial;
 KW CD8 agonist; vaccine; fibrosarcoma; cancer; infectious disease;
 KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
 KW antibody B11; heavy chain variable region.
 XX Homo sapiens.
 PN WO2004074432-A2.
 XX PD 02-SEP-2004.
 XX PR 30-JAN-2004; 2004WO-US002725.
 PR 31-JAN-2003; 2003US-0443979P.
 XX PA (MEDA-) MEDAREX INC.
 XX PI Keler T, Endres M, He L, Ramakrishna V;
 XX DR WPI: 2004-635555/61.
 DR N-PSDB; ADR46820.

XX New molecular conjugate having a monoclonal antibody that binds to human PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a PT cytotoxic T cell response in cancers and infectious diseases.

XX Claim 11; SEQ ID NO 4; 82pp; English.

The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to a human antigen presenting Cells (APCs) linked to beta human chorionic gonadotropin (betahCG), where the antibody comprises a heavy and/or light chain variable region derived from a human VH5-51 or VK-L15 germline sequence with the 98 or 95 amino acid sequences of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are linked to betahCG; (2) a molecular conjugate comprising a human single chain antibody that binds to human APCs linked to betahCG, where the conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an adjuvant; (4) inducing or enhancing a T cell-mediated immune response, comprising contacting any of the molecular conjugates described above with APCs such that the antigen is processed and presented to T cells in a manner which induces or enhances a T cell-mediated response against the antigen; (5) immunising a subject comprising administering any of the molecular conjugates described above, comprising in combination with an adjuvant, a cytokine which stimulates proliferation of dendritic cells and/or an immunostimulatory agent; and (6) inducing or enhancing a cytotoxic T cell response against an antigen, comprising forming conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either in vivo or ex vivo with APCs such that the antigen is internalised, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate has cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic, virucide and antimarial activities, and can be used as a CD8 agonist, and in vaccines. The methods and compositions of the present invention are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents a human antibody B11 heavy chain variable region, which is used in the exemplification of the present invention.

XX Sequence 116 AA;

Query Match Score 621; DB 8; Length 116;
 Best Local Similarity 100.0%; Pred. No. 7.2e-50;
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRLSCKGSQDSFTTYIGWVRQMPGKGLEWMMGIYPGDSDTIY 60
 Db 1 EVQLVQSGAEVKKPGESLRLSCKGSQDSFTTYIGWVRQMPGKGLEWMMGIYPGDSDTIY 60

Qy 61 SPSFQQVTISADKSISTAYLQWSSLKLASDTSAMYCTRDGVYDYGQTLVTVSS 116
 Db 61 SPSFQQVTISADKSISTAYLQWSSLKLASDTSAMYCTRDGVYDYGQTLVTVSS 116

RESULT 3
 ADR46829
 ID ADR46829 standard; protein; 411 AA.
 XX
 AC ADR46829;
 DT 18-NOV-2004 (first entry)

XX Human PB11-betahCG molecular conjugate protein SEQ ID NO:12.
 KW molecular conjugate; monoclonal antibody; human antigen presenting cell;
 KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
 KW betahCG; beta chorionic gonadotropin; antibody; human chorionic gonadotropin;

KW T cell-mediated immune response; immunisation; cytototoxic; antimicrobial;
 KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
 KW CDB agonist; vaccine; autoimmune disorder; cancer; infectious disease;
 KW melanoma; fibrosarcoma; leukemia; HIV; hepatitis; malaria; herpes;
 KW antibody B11; pb11-betaNG molecular conjugate; fusion protein.
 XX Homo sapiens.
 OS Synthetic.
 XX WO2004074432-A2.
 XX PD 02-SEP-2004.
 XX PA 30-JAN-2004; 2004WO-US002725.
 XX PR 31-JAN-2003; 2003US-0443979P.
 XX PA (MEDA-) MEDAREX INC.
 XX PI Keler T, Endres M, He L, Ramakrishna V;
 XX WPI: 2004-635555/61.
 XX N-PSDB; ADR46848.
 XX New molecular conjugate having a monoclonal antibody that binds to human
 PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a
 PT cytotoxic T cell response in cancers and infectious diseases.
 XX PS Claim 16; SEQ ID NO 12; 82pp; English.
 XX CC The present invention describes a molecular conjugate comprising a
 CC monoclonal antibody that binds to human antigen presenting cells (APCs)
 CC linked to beta human chorionic gonadotropin (betahCG), where the antibody
 CC comprises a heavy and/or light chain variable region derived from a human
 CC VH5-1 or VK-L15 germline sequence with the 98 or 95 amino acid sequences
 CC of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
 CC described: (1) a molecular conjugate comprising a human antibody heavy
 CC chain and a human antibody light chain, where either or both chains are
 CC linked to betaNGC; (2) a molecular conjugate comprising a human single
 CC chain antibody that binds to human APCs linked to betahCG, where the
 CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
 CC (ADR46829); (3) a composition comprising any of the molecular conjugates
 CC as described above, and a carrier, optionally in combination with an
 CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
 CC against betahCG, comprising contacting any of the molecular conjugates
 CC described above with APCs such that the antigen is processed and
 CC presented to T cells in a manner which induces or enhances a T cell-
 CC mediated response against the antigen; (5) immunising a subject
 CC comprising administering any of the molecular conjugates described above,
 CC optionally in combination with an adjuvant, a cytokine which stimulates
 CC proliferation of dendritic cells and/or an immunostimulatory agent; and
 CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,
 CC comprising forming a conjugate of the antigen and a monoclonal antibody
 CC which binds to APCs, and contacting the conjugate either in vivo or ex
 CC vivo with APCs such that the antigen is internalised, processed and
 CC presented to T cells in a manner which induces or enhances a cytotoxic T
 CC cell response against the antigen. The molecular conjugate has
 CC cytotoxic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
 CC virucide and antimalarial activities, and can be used as a CDB agonist,
 CC and in vaccines. The methods and compositions of the present invention
 CC are useful for inducing a cytotoxic T cell response, and in particular
 CC for treating autoimmune disorders, cancers and infectious diseases by
 CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
 CC including melanoma, fibrosarcoma, leukemia, HIV, hepatitis, malaria and
 CC herpes. The present sequence represents a human pb11-betaNG molecular
 CC conjugate, which is used in the exemplification of the present invention.
 XX SQ Sequence 411 AA;

Query Match 100.0%; Score 621; DB 8; Length 411;
 Best Local Similarity 100.0%; Pred. No. 2.7e-49;
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPGESELRSICKGSGDSFTTYIGWVRMGPKGLEMGGIYPGSDPTV 60
 Db 142 EVQLVQSGAEVKKPGESELRSICKGSGDSFTTYIGWVRMGPKGLEMGGIYPGSDPTV 201
 QY 61 SPSFPGQVTISADKSISIAYLQWSLKAASDAMYCTRGDVGTYWGQSTLVTVSS 116
 Db 202 SPSFPGQVTISADKSISIAYLQWSLKAASDAMYCTRGDVGTYWGQSTLVTVSS 257

RESULT 4
 ADR46819
 ID ADR46819 standard; protein; 468 AA.

XX AC ADR46819;

XX DT 18-NOV-2004 (first entry)

DB Human antibody B11 heavy chain variable region protein SEQ ID NO:2.

XX DE KW molecular conjugate; monoclonal antibody; human antigen presenting cell;
 PI KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
 XX KW betahCG; beta chorionic gonadotropin; antibody;
 DR KW T cell-mediated immune response; immunisation; cytotoxic; antimicrobial;
 XX KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
 PT KW CDB agonist; vaccine; autoimmune disorder; cancer; infectious disease;
 PT KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
 PT KW antibody B11; heavy chain variable region.

XX OS Homo sapiens.

PN WO2004074432-A2.

PN PN WO2004074432-A2.

XX PD 02-SEP-2004.

XX PR 30-JAN-2004; 2004WO-US002725.

XX PR 31-JAN-2003; 2003US-0443979P.

XX PA (MEDA-) MEDAREX INC.

XX PI Keller T, Endres M, He L, Ramakrishna V;

XX DR WPI: 2004-635555/61.

XX DR N-PSDB; ADR46818.

XX PT New molecular conjugate having a monoclonal antibody that binds to human
 PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a
 PT cytotoxic T cell response in cancers and infectious diseases.

XX PA Claim 13; SEQ ID NO 2; 82pp; English.

XX CC The present invention describes a molecular conjugate comprising a
 CC monoclonal antibody that binds to human antigen presenting cells (APCs),
 CC linked to beta human chorionic gonadotropin (betahCG), where the antibody
 CC comprises a heavy and/or light chain variable region derived from a human
 CC VH5-1 or VK-L15 germline sequence with the 98 or 95 amino acid sequences
 CC of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
 CC described: (1) a molecular conjugate comprising the 411 amino acid sequence
 CC of SEQ ID NO:30 or 32 (ADR46829); (2) a composition comprising any of the molecular conjugates
 CC as described above, and a carrier, optionally in combination with an
 CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
 CC against betahCG, comprising contacting any of the molecular conjugates
 CC described above with APCs such that the antigen is processed and
 CC presented to T cells in a manner which induces or enhances a T cell-
 CC mediated response against the antigen; (5) immunising a subject
 CC comprising administering any of the molecular conjugates described above,
 CC optionally in combination with an adjuvant, a cytokine which stimulates
 CC proliferation of dendritic cells and/or an immunostimulatory agent; and
 CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,
 CC comprising forming a conjugate of the antigen and a monoclonal antibody
 CC which binds to APCs, and contacting the conjugate either in vivo or ex
 CC vivo with APCs such that the antigen is internalised, processed and
 CC presented to T cells in a manner which induces or enhances a cytotoxic T
 CC cell response against the antigen. The molecular conjugate has
 CC cytotoxic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
 CC virucide and antimalarial activities, and can be used as a CDB agonist,
 CC and in vaccines. The methods and compositions of the present invention
 CC are useful for inducing a cytotoxic T cell response, and in particular
 CC for treating autoimmune disorders, cancers and infectious diseases by
 CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
 CC including melanoma, fibrosarcoma, leukemia, HIV, hepatitis, malaria and
 CC herpes. The present sequence represents a human pb11-betaNG molecular
 CC conjugate, which is used in the exemplification of the present invention.
 XX SQ Sequence 411 AA;

CC comprising administering any of the molecular conjugates described above,
 CC optionally in combination with an adjuvant, a cytokine which stimulates
 CC proliferation of dendritic cells and/or an immunostimulatory agent; and
 CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,

comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either *in vivo* or *ex vivo* with APCs such that the antigen is internalised, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate has cytosolic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic, virucide and antimalarial activities, and can be used as a CD8 agonist, and in vaccines. The methods and compositions of the present invention are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents a human antibody B11 heavy chain variable region, which is used in the exemplification of the present invention.

XX Sequence 468 AA;

Query Match	Score	DB	Length
Best Local Similarity	100.0%	621	468;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy 1 EVQLVQSAEVYKPGESLRISCKGSDSFTTYWIGVRQMPGKGLEWMGIYPGDSDTIY 60			
Db 20 EVQLVQSAEVYKPGESLRISCKGSDSFTTYWIGVRQMPGKGLEWMGIYPGDSDTIY 79			
Qy 61 SPSFQQVTISADKSISTAYLQWSSLIKASDAMYCTRGDRGVDTWQGQTLVTVSS 116			
Db 80 SPSFQQVTISADKSISTAYLQWSSLIKASDAMYCTRGDRGVDTWQGQTLVTVSS 135			

RESULT 5
ADR46827 ID ADR46827 standard; protein; 613 AA.
AC ADR46827;
DT 18-NOV-2004 (first entry)
XX Human batchCG-B11 molecular conjugate protein SBQ ID NO:10.

XX molecular conjugate; monoclonal antibody; human antigen presenting cell; antigen presenting cell; APC; human; beta human chorionic gonadotropin; betacG; beta chorionic gonadotropin; antibody; T cell-mediated immune response; immunotherapy; cytostatic; antimicrobial; immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial; CD8 agonist; autoimmune disorder; cancer; infectious disease; melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes; antibody B11; betacG-B11 molecular conjugate; fusion protein.
OS Homo sapiens.
OS Synthetic.

XX WO2004074432-A2.

XX 02-SEP-2004.
XX 30-JAN-2004; 2004WO-US002725.

XX 31-JAN-2003; 2003US-0443979P.

XX (MEDA-) MEDAREX INC.

XX Keler T, Endres M, He L, Ramakrishna V;

XX WPI: 2004-635555/61.

DR N-PSDB; ADR46826.

XX New molecular conjugate having a monoclonal antibody that binds to human APCs linked to a beta human chorionic Gonadotropin, useful for inducing a cytotoxic T cell response in cancers and infectious diseases.
XX Example 1; SEQ ID NO 10; 82pp; English.

XX The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (APCs) linked to beta human chorionic gonadotropin (batchCG), where the antibody comprises a heavy and/or light chain variable region derived from a human VH551 or VK-115 germline sequence with the 98 or 95 amino acid sequences of SBQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are linked to batchCG; (2) a molecular conjugate comprising a human single chain antibody that binds to human APCs linked to batchCG, where the conjugate comprises the 411 amino acid sequence of SBQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an adjuvant; (4) inducing or enhancing a T cell-mediated immune response, against batchCG, comprising contacting any of the molecular conjugates described above with APCs such that the antigen is processed and presented to T cells in a manner which induces or enhances a T cell-mediated response against the antigen; (5) immunising a subject described above, comprising administering any of the molecular conjugates described above, in combination with an adjuvant, a cytokine which stimulates proliferation of dendritic cells and/or an immunostimulatory agent; and (6) inducing or enhancing a cytotoxic T cell response against an antigen, comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either *in vivo* or *ex vivo* with APCs such that the antigen is internalised. Processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate has cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic, virucide and antimalarial activities, and can be used as a CD8 agonist, and in vaccines. The methods and compositions of the present invention are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents a human batchCG-B11 molecular conjugate. The present sequence is used in the exemplification of the present invention.

SQ Sequence 613 AA;

Query Match	Score	DB	Length
Best Local Similarity	100.0%	621	613;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy 1 EVQLVQSAEVYKPGESLRISCKGSDSFTTYWIGVRQMPGKGLEWMGIYPGDSDTIY 60			
Db 20 EVQLVQSAEVYKPGESLRISCKGSDSFTTYWIGVRQMPGKGLEWMGIYPGDSDTIY 79			
Qy 61 SPSFQQVTISADKSISTAYLQWSSLIKASDAMYCTRGDRGVDTWQGQTLVTVSS 116			
Db 80 SPSFQQVTISADKSISTAYLQWSSLIKASDAMYCTRGDRGVDTWQGQTLVTVSS 135			

Query Match 100.0%; Score 621; DB 8; Length 613;
Best Local Similarity 100.0%; Pred. No. 4 1e-49;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVQLVQSAEVYKPGESLRISCKGSDSFTTYWIGVRQMPGKGLEWMGIYPGDSDTIY 60
Db 20 EVQLVQSAEVYKPGESLRISCKGSDSFTTYWIGVRQMPGKGLEWMGIYPGDSDTIY 79
Qy 61 SPSFQQVTISADKSISTAYLQWSSLIKASDAMYCTRGDRGVDTWQGQTLVTVSS 116
Db 80 SPSFQQVTISADKSISTAYLQWSSLIKASDAMYCTRGDRGVDTWQGQTLVTVSS 135

RESULT 6
ADR47223 ID ADR47223 standard; protein; 117 AA.
AC ADR47223;
DT 09-SEP-2004 (first entry)
XX Human phospholipase A2-specific monoclonal antibody heavy chain #21.
XX human; monoclonal antibody; phospholipase A2; PLA2;
XX inflammatory disorder; degenerative disorder;
XX joint inflammatory reaction; skin inflammatory reaction;
XX blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
XX Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
XX Homo sapiens.
XX WO2004050850-A2.

CC The invention comprises a human monoclonal antibody that binds to
 CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
 CC useful in the preparation of a medicament for the treatment of inflammatory
 CC and degenerative disorders stemming from inflammatory
 CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
 CC Alzheimer's disease, atherosclerosis, and restenosis. The present
 CC amino acid sequence represents the heavy chain from a monoclonal antibody
 CC that is specific for the human phospholipase A2 (PLA2) enzyme.

XX Sequence 117 AA;

```
Query Match          89.9%; Score 558; DB 8; Length 117;
Best Local Similarity 91.4%; Pred. No. 5.1e-44;
Matches 106; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
Qy   1 EVQLVQSAEVKKPGEISLRLSCKGSDSFTTYWIGVRQMPGKGLEWMGIIYPGDSDTIY 60
Db    1 EVQLVQSAEVKKPGEISLRLSCKGSDSFTTYWIGVRQMPGKGLEWMGIIYPGDSDTIY 60
Qy   61 SPSFQQTISADKSISTAYLQWSSLKASDAMYCTRGDRGVDTWQGTLVTYSS 116
Db    61 SPSFQQTISADKSISTAYLQWSSLKASDAMYCTRGDRGVDTWQGTLVTYSS 116
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RESULT 9

ID AAW27555 Standard; protein; 120 AA.

XX AC AAW27555;

XX DT 23-JAN-1998 (First entry)

XX DE Human Ab heavy chain variable region VH5 consensus.

XX KW Human; antibody; preparation; library; VH5; variable region; heavy chain;

XX consensus.

XX OS Homo sapiens.

XX PN WO9708320-A1.

XX PD 06-MAR-1997.

XX PF 19-AUG-1996; 96WO-EP003647.

XX PR 18-AUG-1995; 95EP-00113021.

XX PA (MORPHOSYS) GES PROTEINOPTIMIZING MBH.

XX PI Knappik A, Pack P, Ilag V, Ge L, Moroney S, Plueckthun A;

XX WPI; 1997-179277/16.

XX N-PSDB; AAT87933.

XX Preparation of human derived antibody gene library - using synthetic
 PT consensus sequences, and signal consensus antibody gene as universal
 PT framework for highly diverse antibody libraries.
 XX Example 1; Fig 5F; 436pp; English.

CC The present sequence is the human antibody heavy chain variable region
 CC synthetic sequence VH5, used in the preparation of a human derived
 CC antibody gene library.

XX Sequence 120 AA;

```
Query Match          89.5%; Score 556; DB 6; Length 120;
Best Local Similarity 89.2%; Pred. No. 8e-44;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;
Qy   1 EVQLVQSAEVKKPGEISLRLSCKGSDSFTTYWIGVRQMPGKGLEWMGIIYPGDSDTIY 60
Db    1 EVQLVQSAEVKKPGEISLRLSCKGSDSFTTYWIGVRQMPGKGLEWMGIIYPGDSDTIY 60
Qy   61 SPSFQQTISADKSISTAYLQWSSLKASDAMYCTRGDRGVDTWQGTLVTYSS 116
Db    61 SPSFQQTISADKSISTAYLQWSSLKASDAMYCARNGGDGFYAMDYGQGTIVTVSS 120
```

CC 61 SPSFQQTISADKSISTAYLQWSSLKASDAMYCTR---GDRGVDTWQGTLVTYSS 116
 CC 61 SPSFQQTISADKSISTAYLQWSSLKASDAMYCARNGGDGFYAMDYGQGTIVTVSS 120

RESULT 10

ID ABJ18677 Standard; protein; 120 AA.

XX AC ABJ18677;

XX DT 06-MAR-2003 (first entry)

XX DE Antibody library related heavy variable chain protein region SEQ ID No 6.

XX KW Library; recombinant antibody; clustering variable region; in silico;

XX KW immunogenecity; antibody therapeutic.

XX Unidentified.

OS WO2002842277-A1.

XX PN WO2002842277-A1.

XX PD 24-OCT-2002.

XX PF 17-APR-2002; 2002WO-US012202.

XX PR 17-APR-2001; 2001US-0284407P.

XX PA (ABMA-) ABMAXIS INC.

XX PI Luo P;

XX DR WPI; 2003-093043/08.

XX Disclosure; Page 102-103; 119pp; English.

XX PT Constructing a library of recombinant antibodies useful as source of

PT antibody candidates for screening antigens comprises clustering variable

PT regions of antibodies having known 3-dimensional structures into

PT structural ensembles.

XX PT Disclosure; Page 102-103; 119pp; English.

XX CC The invention relates to a novel method for the construction of a library

CC of recombinant antibodies. The novel method comprises clustering variable

CC regions of a collection of antibodies having known 3D structures into at

CC least two families of structural ensembles, each comprising at least two

CC different antibody sequences but with substantially identical main chain

CC conformations. The method is useful for constructing a library of

CC artificial antibodies in silico which provides a structurally diverse and

CC yet functionally more relevant source of antibody candidates which can

CC then be screened for binding a wide variety of target molecules,

CC including small molecules, and biomacromolecules such as proteins,

CC peptides and nucleic acids. The libraries constructed are useful as a

CC source of antibody candidates for further screening for novel antibodies

CC with high affinity against a wide range of antigens and having no or

CC minimum immunogenicity to human subjects treated with antibody

CC therapeutics. This sequence represents a protein region of an antibody

CC relating to the novel antibody library construction method of the

CC invention.

XX SQ Sequence 120 AA;

Query Match 89.5%; Score 556; DB 6; Length 120;
 Best Local Similarity 89.2%; Pred. No. 8e-44;
 Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

Qy 1 EVQLVQSAEVKKPGEISLRLSCKGSDSFTTYWIGVRQMPGKGLEWMGIIYPGDSDTIY 60

Db 1 EVQLVQSAEVKKPGEISLRLSCKGSDSFTTYWIGVRQMPGKGLEWMGIIYPGDSDTIY 60

Qy 61 SPSFQQTISADKSISTAYLQWSSLKASDAMYCTRGDRGVDTWQGTLVTYSS 116

Db 61 SPSFQQTISADKSISTAYLQWSSLKASDAMYCARNGGDGFYAMDYGQGTIVTVSS 120

RESULT 11

ID ABJ18720 standard; protein; 120 AA.
 XX
 AC ABJ18720;
 XX DT 06-MAR-2003 (first entry)
 DB Antibody library related VH protein region 1DHW.
 XX
 KW Library; recombinant antibody; clustering variable region; in silico;
 immunogenicity; antibody therapeutic.
 XX OS Unidentified.
 XX PN WO200284277-A1.
 XX PD 24-OCT-2002.
 XX PF 17-APR-2002; 2002WO-US012202.
 XX PR 17-APR-2001; 2001US-0284407P.
 XX PA (ABMA-) ABMAXIS INC.
 XX PI Luo P;
 XX DR; 2003-093043/08.
 XX PT Constructing a library of recombinant antibodies useful as source of
 antibody candidates for screening antigens comprises clustering variable
 regions of antibodies having known 3-dimensional structures into
 structural ensembles.
 XX Disclosure; Fig 13B; 119PP; English.

The invention relates to a novel method for the construction of a library of recombinant antibodies. The novel method comprises clustering variable regions of a collection of antibodies having known 3D structures into at least two families of structural ensembles, each comprising at least two different antibody sequences but with substantially identical main chain conformations. The method is useful for constructing a library of artificial antibodies in silico which provides a structurally diverse and yet functionally more relevant source of antibody candidates which can then be screened for binding a wide variety of target molecules, including small molecules, and biomacromolecules such as proteins, peptides and nucleic acids. The libraries constructed are useful as a source of antibody candidates for further screening for novel antibodies with high affinity against a wide range of antigens and having no or minimum immunogenicity to human subjects treated with antibody therapeutics. This sequence represents a protein region of an antibody relating to the novel antibody library construction method of the invention.

XX Sequence 120 AA;

Query Match 89.5%; Score 556; DB 6; Length 120;

Best Local Similarity 89.2%; Pred. No. 8e-44; Mismatches 3; Indels 4; Gaps 1;

SQ Sequence 252 AA;

Query Match 89.0%; Score 552.5; DB 5; Length 252;

Best Local Similarity 84.8%; Pred. No. 3.7e-43; Mismatches 4; Indels 6; Gaps 9;

SQ :

Db 1 EVQLVQSGAEVKKPGESLRISCKSGDSFTTYWIGVRQMPGKGLEMGIIYPGDSDPTIY 60

Db 1 EVQLVQSGAEVKKPGESLRISCKSGDSFTSYWIGVRQMPGKGLEMGIIYPGDSDPTIY 60

Qy 61 SPSFQGQVTISADKSISPAYLQNSLKSADTAMYCPR---GDRGYDLYWGCGTLYTVSS 116

Db 61 SPSFQGQVTISADKSISPAYLQNSLKSADTAMYCPR---GDRGYDLYWGCGTLYTVSS 120

Qy 61 SPSFQGQVTISADKSISPAYLQNSLKSADTAMYCRLDYDILTGYPGSGFDYWGQGT 111

Db 61 SPSFQGQVTISADKSISPAYLQNSLKSADTAMYCRLDYDILTGYPGSGFDYWGQGT 120

RESULT 12
 ABP45526

ID ABP45526 standard; protein; 252 AA.

XX AC ABP45526;

XX DT 19-AUG-2002 (first entry)

XX Human BLyS binding scFv SEQ ID 1537.

DE Human BLyS binding scFv SEQ ID 1537.
 XX BLyS; B lymphocyte stimulator; TNF superfamily; human; cycostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; anti-rheumatic;
 KW anti-AIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX OS Homo sapiens.

XX PN WO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0211210P.

XX PR 17-OCT-2000; 2000US-0244816P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0277379P.

XX PR 25-MAY-2001; 2001US-0293499P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX DR WPI; 2002-114799/15.

XX PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX PT Claim 1; Page 2237-2238; 3148PP; English.
 XX PS This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunomodulatory,
 CC antirheumatic and anti-ANS activity and can be used in vaccines to
 CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
 CC and so may be used to detect and quantitate the presence of BLyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BLyS. They may also be
 CC administered to treat diseases associated with aberrant BLyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention

XX SQ Sequence 252 AA;

Query Match 89.0%; Score 552.5; DB 5; Length 252;

Best Local Similarity 84.8%; Pred. No. 3.7e-43; Mismatches 4; Indels 6; Gaps 9;

Matches 106; Conservative 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKSGDSFTTYWIGVRQMPGKGLEMGIIYPGDSDPTIY 60

Db 1 QVQLVQSGAEVKKPGESLRISCKSGDSFTSYWIGVRQMPGKGLEMGIIYPGDSDPTIY 60

Qy 61 SPSFQGQVTISADKSISPAYLQNSLKSADTAMYCPR---GDRGYDLYWGCGTLYTVSS 116

Db 61 SPSFQGQVTISADKSISPAYLQNSLKSADTAMYCPR---GDRGYDLYWGCGTLYTVSS 120

Qy 61 SPSFQGQVTISADKSISPAYLQNSLKSADTAMYCRLDYDILTGYPGSGFDYWGQGT 111

Db 61 SPSFQGQVTISADKSISPAYLQNSLKSADTAMYCRLDYDILTGYPGSGFDYWGQGT 120

Qy	112	VTVSS 116	1	EVQLVQSGAEVKPQEBSLRISCKSGDSFTTYWIGVROMP GKLSLWMGILYTPGSDDTIV 60
Db	121	VTVSS 125	1	QVQLVQSGAEVKPQEBSLRISCKSGDSFTSYWIGVROMP GKLSLWMGILYTPGSDDTIV 60
RESULT 13				
ID ADG96353				
XX	ADG96353 standard; protein; 252 AA.			
XX	AC ADG96353;			
DT 11-MAR-2004	(first entry)			
DE Single chain antibody that immunospecifically binds BlyS SeqID 1537.				
XX	KW antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;			
XX	B cell proliferation; differentiation; scFv; myasthenia gravis;			
XX	multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;			
XX	carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;			
XX	antiinflammatory; antiasthmatic; antiallergic; cytostatic.			
XX	Unidentified.			
XX	WO2003055979-A2.			
XX	PS 10-JUL-2003.			
XX	PF 14-NOV-2002; 2002WO-US036496.			
XX	PR 16-NOV-2001; 2001US-0331469P.			
XX	PR 19-DEC-2001; 2001US-0340817P.			
XX	PA (HUM-) HUMAN GENOME SCI INC.			
XX	PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;			
XX	DR WPI; 2003-505530/47.			
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BlyS), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.				
XX	PS Example 1; SEQ ID NO 1537; 39pp; English.			
XX	This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to chromosome 13q34 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BlyS. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BlyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiarthritic, neuroprotective, antiinflammatory, antiasthmatic, antiallergic and cytostatic. This polypeptide sequence is a single chain antibody that binds BlyS of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pct_sequences .			
XX	Sequence 252 AA;			
SQ	89.0%; Score 552.5; DB 7; Length 252;			
Best Local Similarity 84.8%; Pred. No. 3.7e-43; Matches 106; Conservative 4; Mismatches 6; Indels 9; Gaps 1;				
Query Match 89.0%; Score 552.5; DB 8; Length 266;				
Best Local Similarity 88.4%; Pred. No. 3.9e-43; Matches 107; Conservative 2; Mismatches 7; Indels 5; Gaps 1;				

Qy 1 EYOLVQSAEVKPGESLRISCKGSDFTTWIGMVRQMPGKGLEWMGILYPGDSDTIY 60
 Db 12 EYOLVQSAEVKPGESLRISCKGSDFTTWIGMVRQMPGKGLEWMGILYPGDSDTIY 71

Qy 61 SPSFQQVTISADKSISSTAYLQSSLKASDTAMYCTR-----GDRGVDFYNGQFTLVTS 115
 Db 72 SPSFQQVTISADKSISSTAYLQSSLKASDTAMYCTR-----GDRGVDFYNGQFTLVTS 131

Qy 116 S 116
 Db 132 S 132

RESULT 15

ADP47229

ID ADP47229 standard; protein; 117 AA.

XX

AC ADP47229;

XX

DT 09-SEP-2004 (first entry)

DB Human phospholipase A2-specific monoclonal antibody heavy chain #27.

XX

KW human; monoclonal antibody; phospholipase A2; PLA2;

KW inflammatory disorder; degenerative disorder;

KW joint inflammatory reaction; skin inflammatory reaction;

KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;

KW Alzheimer's disease; atherosclerosis; restenosis; heavy chain.

OS Homo sapiens.

XX

PN WO2004050850-A2.

XX

PD 17-JUN-2004.

XX

PP 02-DEC-2003; 2003WO-US038234.

XX

PR 02-DEC-2002; 2002US-0430724P.

XX

PA (ABGENIX INC.

PA (LEXI-)

LEXICON GENETICS INC.

XX

PT Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang MI, Feng X;

PT Jia X, Nocerini MR;

XX

DR WPI; 2004-161119/43.

XX

PT New human monoclonal antibody that binds to phospholipase A2 (PLA2),

PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,

PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.

XX

PS Example 5; SEQ ID NO 144; 128pp; English.

XX

CC The invention comprises a human monoclonal antibody that binds to

CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is

CC useful in the preparation of a medicament for the treatment of

CC inflammatory and degenerative disorders stemming from inflammatory

CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,

CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present

CC amino acid sequence represents the heavy chain from a monoclonal antibody

CC that is specific for the human phospholipase A2 (PLA2) enzyme.

XX

SQ Sequence 117 AA:

Query Match 88.9%; Score 552; DB 8; Length 117;

Best Local Similarity 89.7%; Pred. No. 1, Be-43;

Matches 104; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 EYOLVQSAEVKPGESLRISCKGSDFTTWIGMVRQMPGKGLEWMGILYPGDSDTIY 60

Db 1 EYOLVQSAEVKPGESLRISCKGSDFTTWIGMVRQMPGKGLEWMGILYPGDSDTIY 60

Qy 61 SPSFQQVTISADKSISSTAYLQSSLKASDTAMYCTR-----GDRGVDFYNGQFTLVTS 116

Qy 1 EYOLVQSAEVKPGESLRISCKGSDFTTWIGMVRQMPGKGLEWMGILYPGDSDTIY 60
 Db 12 EYOLVQSAEVKPGESLRISCKGSDFTTWIGMVRQMPGKGLEWMGILYPGDSDTIY 71

Qy 61 SPSFQQVTISADKSISSTAYLQSSLKASDTAMYCTR-----GDRGVDFYNGQFTLVTS 115
 Db 72 SPSFQQVTISADKSISSTAYLQSSLKASDTAMYCTR-----GDRGVDFYNGQFTLVTS 131

Qy 116 S 116
 Db 132 S 132

Search completed: December 3, 2005, 14:25:01
 Job time : 200.384 secs

Db 61 SPSFQQVTISADKSISSTAYLQSSLKASDTAMYCTR-----GDRGVDFYNGQFTLVTS 116

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Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6									
OM protein - protein search, using sw model										
Run on: December 3, 2005, 14:11:48 ; Search time 204.539 Seconds (without alignments)	400.126 Million cell updates/sec									
Title: Perfect score: 621	US-10-769-144-4									
Sequence: 1 EVQLVQSGAEVTKPGESELRII.....TRGDRGVYDYGCGTIVTSS 116										
Scoring table: BL05UM62										
Searched: 2166443 seqs, 705528306 residues	Total number of hits satisfying chosen parameters: 2166443									
Minimum DB seq length: 0	Maximum DB seq length: 2000000000									
Post-processing: Minimum Match 0%	Maximum Match 100%									
Database : UniProt 05.80:*	Listing first 45 summaries									
1: uniprot_sprot:*										
2: uniprot_trembl:*										
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.										
SUMMARIES										
Result No.	Score	Query Match	Length	DB ID	Description					
1	4.34	69.9	475	2	QSREB17_PONY					
2	3.89	62.6	124	2	Q9UL92_HUMAN					
3	3.81.5	61.4	119	2	Q9UL94_HUMAN					
4	3.79	61.0	118	2	Q9Z1C4_MOUSE					
5	3.79	61.0	590	2	Q4V9V8_MOUSE					
6	3.74.5	60.3	614	2	Q7TM76_MOUSE					
7	3.72.5	60.0	244	2	Q6SZC8_HUMAN					
8	3.72	60.0	481	2	Q9LWT1_HUMAN					
9	3.72	59.9	498	2	Q6N041_HUMAN					
10	3.69.5	59.5	458	2	QSBJZ2_RAT					
11	3.67.5	59.2	125	2	Q9DU95_HUMAN					
12	3.66.5	59.0	473	2	Q9PB44_MOUSE					
13	3.62.5	58.4	480	2	Q6P089_HUMAN					
14	3.59	57.8	116	2	Q9U189_HUMAN					
15	3.58.5	57.7	146	2	Q9Z4Q3_MOUSE					
16	3.58.5	57.7	616	2	Q5O4M7_MOUSE					
17	3.58	57.6	518	2	Q6N030_HUMAN					
18	3.57.5	57.6	125	1	HV1F_HUMAN					
19	3.56.5	57.4	120	2	Q5F2T1_MOUSE					
20	3.56	57.3	143	2	Q9A4Q0_MOUSE					
21	3.56	57.3	617	2	Q4RML5_MOUSE					
22	3.55	57.2	159	2	Q9E0S0_HUMAN					
23	3.55	57.2	482	2	Q8K172_MOUSE					
24	3.54.5	57.1	119	2	Q9GY22_MOUSE					
25	3.54.5	57.1	142	2	Q9Z4Q1_MOUSE					
26	3.54.5	57.1	464	2	Q6PP95_MOUSE					
27	3.54.5	57.1	483	2	Q52151_MOUSE					
28	3.54	57.0	143	2	Q9Z4R0_MOUSE					
29	3.53	56.9	519	2	Q5BBM2_HUMAN					
30	3.53	56.8	141	2	Q9Z4Q4_MOUSE					
31	3.53	56.8	145	2	Q9Z4R4_MOUSE					

ALIGNMENTS

RESULT 1
QSREB17_PONY PRELIMINARY;
ID QSREB17_PONY PRELIMINARY;
AC QSREB17;
DT 01-FEB-2005 (TREMBrel. 29, Created)
DT 01-FEB-2005 (TREMBrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBrel. 29, Last annotation update)
DB Hypothetical protein DKFP465C2335.
GN Name=DKFP465C2335;
RN Pongo pygmaeus (Orangutan).
RC TISSUE=Kidney;
RA The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR857722; CAB89990.1; ; mRNA.
DR SMR; QSREB17; 21-475.
DR GO; GO:00310106; P:PMC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen via . . . ; IEA.
DR GO; GO:0019885; P:antigen processing, endogenous antigens via . . . ; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set-.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IgCl; 3.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; Ig_LIKE; 4.
DR PROSITE; PS00290; Ig_MHC; UNKNOWN_2.
KW Hypothetical protein.
SEQUENCE 475 AA; 51898 MW; 04BDBE096A2CD529 CRC64;

Query Match Similarity 69.9%; Score 434; DB 2; Length 475;
Best Local Similarity 68.0%; Pred. No. 2.8e-35;
Matches 85; Conservative 13; Mismatches 17; Indels 10; Gaps 2;

Qy 1 EVOVSGAETKPGESLRICKGSDFSFTYYWIGVRQMPGKGILWMGIIYPGDSPTI 60
Db 20 DIQLQSGABYKRPGBSLRICKGSGTFTDYGIGVRQMPGKGILWMGIDPSNSCTKY 79

Qy 61 SPSFGQQTISADKS1STAYLQWSLKAISDTAMYCTR---VDYNGQGT 110
Db 80 NRSFEHIGHITISADM1STAYLQWSLKAISDTAMYCTR---VDYNGQGT 139

Qy 111 LYTVS 115

RESULT 5
Q4V918_MOUSE PRELIMINARY; PRT; 590 AA.
ID Q4V918 ;
AC 04V918 ;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DB Hypothetical protein.
GN Name=1gh-6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus .
NCBI Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubinger R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Sheppard C.M., Schueler G.D.,
RA Altschul S.F., Zeeberg B., Bustow K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Altschul S.F., Zeeberg B., Bustow K.H., Derge J.G., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Jones S.J.M., Marra M.A.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RG NIGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC036667; AAH96667.1; - ; mRNA.
DR MGI; MGI:364448; Ig-h-6.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-11ke.
DR InterPro; IPR003597; Ig-C1.
DR InterPro; IPR003106; Ig-MHC.
DR InterPro; IPR003596; Ig-V.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IgCl; 4.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; Ig_LIKE; 5.
DR PROSITE; PS50835; Ig; 2.
DR PROSITE; PS50835; Ig_MHC; UNKNOWN_3.
DR PROSITE; PS00290; Ig_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ Sequence 590 AA; 64892 MW; D425118F9A188B14 CRC64;
Best Local Similarity 61.0%; **Score** 379; **DB** 2; **Length** 590;
Matches 67; **Conservative** 24; **Mismatches** 25; **Indels** 0; **Gaps** 0;

Query Match 1 EQLVQSGAEVKPGESLRICKGSGDSFTTYWIGNYRQMPGKGLEMNGIYPGDSDTIY 60
Best Local Similarity 57.8%; **Pred.** No. 1.3e-28; **Mismatches** 23; **Indels** 5; **Gaps** 2;
Matches 70; **Conservative** 22; **Mismatches** 23; **Indels** 5; **Gaps** 2;

Qy 1 EQLVQSGAEVKPGESLRICKGSGDSFTTYWIGNYRQMPGKGLEMNGIYPGDSDTIY 60
Db 20 QVQLQQSGPELYVKPGASVKISKASGYAFSSSMNNVKQRPKGLEMIGRYPPGDPDTNY 79
Qy 61 SPSFGQGVITISADSISTAYLQWSLSKASDTPAMYCTTRGDGVD---YWGCGTLYTVSS 116
Db 80 NGKPKGRATLTDQSSTAYMOLSLTSEDAVFCAR-DYGSYXRFAYWGGTLYTVSS 138

RESULT 6
Q7TM76_MOUSE PRELIMINARY; PRT; 614 AA.
ID Q7TM76 ;
AC Q7TM76 ;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DB MGCS0843 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus .
NCBI Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubinger R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Sheppard C.M., Schueler G.D.,
RA Altschul S.F., Zeeberg B., Bustow K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunararne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RA Straubinger R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC033409; AAH963409.1; - ; mRNA.
DR HSSP; P01820; 1G7
DR Ensemble; BNSMUS0000054328; Mus musculus.
DR GO; GO:0003823; F: antigen binding; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; Ig_LIKE; 5.
DR PROSITE; PS00290; Ig_MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ Sequence 614 AA; 67747 MW; 839BAF3BBDD124F89 CRC64;

Query Match 1 EVQLVQSGAEVKPGESLRICKGSGDSFTTYWIGNYRQMPGKGLEMNGIYPGDSDTIY 60
Best Local Similarity 58.3%; **Pred.** No. 3.8e-29; **Mismatches** 23; **Indels** 5; **Gaps** 2;
Matches 70; **Conservative** 22; **Mismatches** 23; **Indels** 5; **Gaps** 2;

Qy 1 EVQLVQSGAEVKPGESLRICKGSGDSFTTYWIGNYRQMPGKGLEMNGIYPGDSDTIY 60
Db 20 QVQLQQSGPELYVKPGASVKISKASGYAFSSSMNNVKQRPKGLEMIGRYPPGDPDTNY 79
Qy 61 SPSFGQGVITISADSISTAYLQWSLSKASDTPAMYCTTRGDGVD---YWGCGTLYTVSS 116
Db 80 NGKPKGRATLTDQSSTAYMOLSLTSEDAVFCAR-DYGSYXRFAYWGGTLYTVSS 138

RESULT 7
Q65ZC8_HUMAN PRELIMINARY; PRT; 244 AA.
ID Q65ZC8 ;

AC Q652C8;	RA Fahay J., Helton B., Madan A., Ketteman M., Rodriguez S., Sanchez A., Whiting M., Madan A. C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.M., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Burrfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E., Scherzer A., Schein J.E., Jones S.J.M., Marra M.A.;
DT 25-OCT-2004 (TREMBUREL 28, Last sequence update)	RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; RT Proc. Natl. Acad. Sci. U.S.A. 99:16893-16903 (2002).
DT 25-OCT-2004 (TREMBUREL 28, Last annotation update)	RN [2]
DE Single-chain Fv (Fragment).	RP NUCLEOTIDE SEQUENCE.
GN Homo sapiens (Human).	RC STRAIN_FVB/N; TISSUE=Colon;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	RA Straubberg R., Submitted (SBP-2001) to the EMBL/GenBank/DDBJ database.
OC NCBI_TAXID=9606;	RL EMBL; BCO13490; ARH13401; -; mRNA.
OX RN [1]	DR HSSP; P01751; 1A6W.
RP NUCLEOTIDE SEQUENCE.	DR Ensembl; ENSMUSG000000021155; Mus musculus.
RX MEDLINE=9262799; PubMed=9219263; DOI=10.1038/nbt0797-629; RA "Complement recruitment using bispecific diabodies.";	DR GO; GO:0003822; P: antigen binding; IEA.
RA Konermann R.E., Wing M.G., Winter G.; DR InterPro; IPR003599; 19.	DR InterPro; IPR007110; Ig-like.
RA Biochemical. 15:629-631(1997).	DR InterPro; IPR003597; Ig CL.
DR EMBL; Y13500; CAAT5500_1; -; mRNA.	DR InterPro; IPR003006; Ig MHC.
DR SMART; SM00406; IgV; 2.	DR InterPro; IPR003596; Ig v.
DR PROSITE; PS50835; Ig_LIKE; 2.	DR Pfam; PF07654; Cl-set; 2.
FT NON_TER 1 1	DR SMART; SM00406; IgV; 1.
FT NON_TER 244 244 AA; 26127 MM; 4B1F1706933882BF CRC64;	DR PROSITE; PS000290; Ig_LIKE; 4.
SQ Sequence 244 AA; 26127 MM; 4B1F1706933882BF CRC64;	DR PROSITE; PS000290; Ig MHC; UNKNOWN_2.
Query Match 60.0%; Score 372.5; DB 2; Length 244;	SQ Sequence 481 AA; 52105 MW; 97DF68D159463F65 CRC64;
Best Local Similarity 57.9%; Pred. No. 2.2e-29;	Query Match 60.0%; Score 372.5; DB 2; Length 481;
Matches 70; Conservative 22; Mismatches 23; Indels 5; Gaps 1;	Best Local Similarity 51.0%; Pred. No. 4.6e-29;
Qy 1 EVQLVQSGAEVKPKGESELISCKGSDFTEYIWMRQPGKGELEMIGIYPGDSDTIV 60	Matches 69; Conservative 23; Mismatches 24; Indels 1; Gaps 1;
Db 1 QVQLVQSGAEVKPKGESELISCKGSDFTEYIWMRQPGKGELEMIGIYPGDSDTIV 60	Qy 1 EVQLVQSGAEVKPKGESELISCKGSDFTEYIWMRQPGKGELEMIGIYPGDSDTIV 60
Qy 61 SPSFGQQVITISADKSISTAYLQWSLSSAKSDTAMYCTGRDR---GVIVWGGTTLTVTS 115	Db 20 QVQLVQSGPVLVKEGASVKSICRASGYTTSYIHWKVRPGQQLWIGMIPGDGNTKV 79
Db 61 AQRFGQVTRMTRDTISAAFMEVSPRLSDTAVYCARFGTGSATYGMWGGTTLTVTS 120	Qy 61 SPSFGQQVITISADKSISTAYLQWSLSSAKSDTAMYCTGRDR-GVIVWGGTTLTVTS 116
Qy 116 S 116	Db 80 NEKFGKTTADKSISSTAYMFLSSLTSDAVYFCTRGGWAFDYWGQSTTLTVTS 136
Db 121 S 121	
RESULT 9	RESULT 9
Q6N041 HUMAN	Q6N041 HUMAN
ID Q6N041; HUMAN PRELIMINARY;	PRT; 498 AA.
AC Q6N041; HUMAN PRELIMINARY;	PRT; 498 AA.
RC TISSUE=Human rectum tumor;	
RC The German Human CDNA Consortium;	
RC Poutka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R., Wiemann S., Mewes H. W., Weil B., Anid C., Osanger A., Fobo G., Han M., Wiemann S., Name=DKEP686O16217;	
RC Submitted (ANG-2003) to the EMBL/GenBank/DDBJ database.	
DR EMBL; B0640710; CAB45829.1; -; mRNA.	
DR HSSP; P01751; 1A6W.	
DR SMR; Q6N041; 268-476.	
DR InterPro; IPR003597; Ig-like.	
DR InterPro; IPR003006; Ig C1.	
DR Pfam; PF07654; Cl-set; 2.	
DR SMART; SM00406; IgV; 4.	
OX NCBI_TaxID=9606;	
OX RN [1]	
RP NUCLEOTIDE SEQUENCE.	
RC TISSUE=Human rectum tumor;	
RC The German Human CDNA Consortium;	
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DR SMART; SM00406; IgV; 4.	
OX NCBI_TaxID=9606;	
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RC TISSUE=Human rectum tumor;	
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RC Poutka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R., Wiemann S., Mewes H. W., Weil B., Anid C., Osanger A., Fobo G., Han M., Wiemann S., Name=DKEP686O16217;	
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DR HSSP; P01751; 1A6W.	
DR SMR; Q6N041; 268-476.	
DR InterPro; IPR003597; Ig-like.	
DR InterPro; IPR003006; Ig C1.	
DR Pfam; PF07654; Cl-set; 2.	
DR SMART; SM00406; IgV; 4.	
OX NCBI_TaxID=9606;	
OX RN [1]	
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RC TISSUE=Human rectum tumor;	
RC The German Human CDNA Consortium;	
RC Poutka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R., Wiemann S., Mewes H. W., Weil B., Anid C., Osanger A., Fobo G., Han M., Wiemann S., Name=DKEP686O16217;	
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DR HSSP; P01751; 1A6W.	
DR SMR; Q6N041; 268-476.	
DR InterPro;	

RESULT 12	Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanuki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsubara S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer." ; [6]
Q9DIL4_MOUSE PRELIMINARY;	PRT; 473 AA.
ID Q9DIL4_	AC DT 01-JUN-2001 (TREMBLrel. 17, Created)
AC DT 01-MAR-2004 (TREMBLrel. 17, Last annotation update)	DE Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched chain of IGM, full insert sequence.
GN Name=Igm-1A;	DE Mammalia: Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Murinae; Mus.
OS Mus musculus (Mouse);	NCBI TaxID=10090;
RN [1]	RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CS7BL/6J; TISSUE=Pancreas;	RX MEDLINE=9927953; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RC Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning." ; [2]	RT "High-efficiency full-length cDNA cloning." ; [2]
RC STRAIN=CS7BL/6J; TISSUE=Pancreas;	RT Meth. Enzymol. 303:19-44(1999).
RC MEDLINE=2108560; PubMed=117851;	RN
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Niizumi K., Kiyosawa H., Kondo S., Yamamoto T., Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R., Kadora K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Giassi C., King B., Kochiwa H., Xuehui P., Lewis S., Matsuo Y., Nakaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono R., Baldarelli R., Barish G., Blake J., Boffelli D., Bolunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fleischer C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sato K., Schoenbach C., Storch K.-P., Tomita M., Tomita M., Suzuki H., Toto-oka K., Wang K.H., Weitz C., Whittaker C., Wilming M., Wynshaw-Boris A., Yoshida K., Hassigawa Y., Kawaji H., Kohzuki S., Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection." ; [3]	
RN [3]	RT "Functional annotation of a full-length mouse cDNA collection." ; [3]
RP NUCLEOTIDE SEQUENCE.	RL Nature 408:685-69 (2001).
RC STRAIN=CS7BL/6J; TISSUE=Pancreas;	RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;	RC STRAIN=CS7BL/6J; TISSUE=Pancreas;
RA Carninci P., Shibata Y., Hayatoku N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes." ; [5]	RA Shibata K., Itoh M., Aizawa K., Naoga S., Sasaki N., Carninci P., Konno H., Akizama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RN [5]	RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=20530913; PubMed=11078861; DOI=10.1101/gr.152600;	RX MEDLINE=20530913; PubMed=11078861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Naoga S., Sasaki N., Carninci P., Konno H., Akizama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,	RA Shibata K., Itoh M., Aizawa K., Naoga S., Sasaki N., Carninci P., Konno H., Akizama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RESULT 13
Q6P089_HUMAN
ID Q6P089_HUMAN PRELIMINARY;

PRT; 480 AA.

AC Q6PQ89; 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DB Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 Homo.
 NCBI_TaxID=9606;
 RN [1] NUCLEOTIDE SEQUENCE.
 RC TISSUE=Glandular pool- thyroid;
 MEDLINE=22388257; PubMed=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derse J.G.,
 Klausner R.D., Colling F.S., Wagner L., Sherman C.M., Schuler G.D.,
 Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Slack M., Soares M.B., Donaldson M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
 Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2] NUCLEOTIDE SEQUENCE.
 RC TISSUE=Glandular pool- thyroid;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DDJB databases.
 DR EMBL; BC055733; AAH55733.1; - ; mRNA.
 DR HSSP; P01751; 1A6W.
 DR SMR; Q6PQ89; 250-458.
 DR InterPro; IPR003599; Ig_1-like.
 DR InterPro; IPR007110; Ig_1-like.
 DR InterPro; IPR003597; Ig_1-cl.
 DR InterPro; IPR003106; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 2.
 DR SMART; SM00409; Ig_4.
 DR SMART; SM00407; Ig_1; 3.
 DR SMART; SM00406; Ig_1v; 1.
 DR PROSITE; PS50835; Ig_LIKE; 4.
 DR PROSITE; PS00290; Ig_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 480 AA; 51997 MW; 2E2B6C57E4F0ED65 CRC64;

Query Match 58.4%; Score 362.5; DB 2; Length 480;
 Best Local Similarity 57.9%; Pred. No. 4.7e-28;
 Matches 70; Conservative 19; Mismatches 27; Indels 5; Gaps 1;

Qy 1 EYLVQSGAEVKPGESLRISKGSGNSFTWIGHYRQMPGKGLEWMGIYPGDSDTIY 60
 20 QVQLVQSGAEVKTGASVSKVSKASGYSISDNYIHWVRQAPQGLEWMMAWRPQNGTVs 79

Db RESULT 15
 61 SPSFQGVITISADKSISTAYLQWSLKLASDAMYCTRGDRG----VTDYNGQGTLYTVS 115
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 80 AEKFQGRVTTIDTSINTAYMELTSIKSDDALYYCARGHSDWSSYYFDYWGQTLVTVs 139

Qy 1 EYLVQSGAEVKPGESLRISKGSGNSFTWIGHYRQMPGKGLEWMGIYPGDSDTIY 60
 20 QVQLVQSGAEVKTGASVSKVSKASGYSISDNYIHWVRQAPQGLEWMMAWRPQNGTVs 79

Db Q924Q3_MOUSE PRELIMINARY; PRT; 146 AA.
 ID Q924Q3; AC Q924Q3; DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DB VH186_2-D_J-C mu protein (Fragment).
 GN Name=VH186_2-D_J-C mu;
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 RN [1] NCB_ TaxID=10090;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
 RN [2] NUCLEOTIDE SEQUENCE.
 RX PubMed=3135311;
 RA Corbet S., Hirn M., Roth C., These J., Pougerau M., Schiff C.;
 RT "Allogeneic manipulation of the GAT idiotypic cascade. Immunization of
 C57BL/6 mice by BALB/C anti-idiotypes stimulates similar strain-
 specific V genes as the original antigen.";
 RL Immunol. 141:779-784 (1988).
 RN [3] NUCLEOTIDE SEQUENCE.
 RP PubMed=2499887;
 RA Baccala R., Quang T. V., Gilbert M., Ternynck T., Avrameas S.;
 RT "Two murine natural polyreactive autoantibodies are encoded by
 nonnucleated germ-line genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).
 DR EMBL; AB067797; BAB3282.1; -; mRNA.
 PIR; F28833; F28833;
 DR PIR; F33932; F33932;
 PIR; PH1105; PH1105;
 DR PIR; PH1108; PH1108;
 PIR; PH1114; PH1114;
 DR PIR; PH1118; PH1118;
 PIR; PH1119; PH1119;
 DR PIR; PH1125; PH1125;
 PIR; PH1126; PH1126;
 DR PIR; PH1128; PH1128;
 PIR; PH1129; PH1129;
 DR PIR; PH1133; PH1133;
 PIR; PH1134; PH1134;
 DR PIR; PH1137; PH1137;
 PIR; PH1139; PH1139;
 DR PIR; PH1142; PH1142;
 PIR; PH1144; PH1144;
 DR PIR; PH1147; PH1147;
 PIR; PH1149; PH1149;
 DR PIR; PH1150; PH1150;
 PIR; PH1151; PH1151;
 DR PIR; PH1152; PH1152;
 PIR; PH1153; PH1153;
 HSSP; P012751; 1AGW.
 DR SMR; Q924Q3; 1-137.
 Ensemble: ENSMUSG00000021155; Mus musculus.
 DR IntePro; IPR007110; Ig-like.
 DR IntePro; IPR003596; Ig_v.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50815; IG_LIKE; 1.
 PT NON_TER 1 1
 FT 146 146
 SQ SEQUENCE 146 AA; 16136 MW; CEA8DD6E1955807F CRC64;
 Query Match 57.7%; Score 358.5; DB 2; Length 146;
 Best Local Similarity 54.5%; Pred. N. 3.3e-28;
 Matches 66; Conservative 21; Mismatches 29; Indels 5; Gaps 1;
 Qy 1 EVQLYSGAEVKPGESLRISCKGSDSFTTYWIGVRQMPGKGLEMMGLIYPGDSDTIV 60
 Db 1 QVQLQQPGAEVLKPGASVLSKACSYTFSYMMHEWVKORGPGLEWIGRIDPNSSGGTVY 60
 Qy 61 SPSFQQVITISADKSISTAVLQWSSLKASDAMIVCTR ---GDRGVDWGQGTIVVS 115
 Db 61 NEKFPSKATLTVDKFSSSTAYMQLSSLTSEDAVYCARSLYDYGDYAMDYWGQGTISVTVS 120
 Qy 116 S 116

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 3, 2005, 14:11:59 ; Search time 31.7224 Seconds
 (without alignments)
 351.837 Million cell updates/sec

Title: US-10-769-144-4
 Perfect score: 621
 Sequence: 1 EvQLVQSGAEVKPKGESSLR1.....TRGDRGVDYWQQGTIVTVSS 116

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : PIR 80-*
 1: Pir1;*
 2: Pir2;*
 3: Pir3;*
 4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	548	88.2	139	2	PH1558		Ig heavy chain V r
2	543.5	87.5	113	2	PH1428		Ig heavy chain V r
3	541.5	87.2	127	2	PH1414		Ig heavy chain V r
4	540.5	87.0	136	2	PH1559		Ig heavy chain V r
5	536.5	86.4	123	2	C36006		Ig heavy chain V r
6	535	86.2	136	2	PH1047		Ig heavy chain V r
7	534.5	86.1	123	2	S38492		Ig heavy chain - h
8	529.5	85.3	127	2	PH1415		Ig heavy chain V r
9	525.5	84.6	123	2	PH1413		Ig heavy chain V r
10	525.5	84.6	127	2	PH1411		Ig heavy chain V r
11	524.5	84.5	123	2	PH1423		Ig heavy chain V r
12	520	83.7	134	2	PH1422		Ig heavy chain V r
13	519.5	83.7	117	2	S19670		Ig heavy chain V r
14	519.5	83.7	127	2	PH1420		Ig heavy chain V r
15	513.5	82.7	117	2	S19669		Ig heavy chain V r
16	510	82.1	137	2	PH1562		Ig heavy chain V r
17	508	81.8	126	2	PH1424		Ig heavy chain V r
18	508	81.8	126	2	PH1419		Ig heavy chain V r
19	505	81.3	126	2	PH1416		Ig heavy chain V r
20	504.5	81.2	138	2	PH1565		Ig heavy chain V r
21	502	80.8	126	2	PH1417		Ig heavy chain V r
22	502	80.8	126	2	PH1418		Ig heavy chain V r
23	500	80.5	126	2	PH1412		Ig heavy chain V r
24	499.5	80.4	125	2	PH1410		Ig heavy chain V r
25	496.5	80.0	138	2	PH1564		Ig heavy chain V r
26	496	79.9	122	2	PH1426		Ig heavy chain V r
27	495	79.7	98	2	S26307		Ig heavy chain V r
28	495	79.7	101	2	S12424		Ig heavy chain V r
29	495	79.7	102	2	PH1279		Ig heavy chain V r

ALIGNMENTS

RESULT 1							
PH1558	19 heavy chain V region (clone DOB)	-	human (fragment)				
C;Species: Homo sapiens (man)							
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 16-Aug-1996							
C;Accession: PH1558							
R;Rosenthal, L.Z.; Kippis, T.J.							
J;Exp. Med. 177, 1039-1046, 1993							
A;Title: Lack of extensive mutations in the VH5 genes used in common B cell chronic lymphoma: immunoglobulin homology <1MM>							
A;Reference number: PH1557; PMID:93210159; PMID:7681468							
A;Molecule type: DNA							
A;Residues: 1-139 <CRAS>							
A;Cross-references: UNIPARC:UPI0000176881							
C;Superfamily: immunoglobulin V region; immunoglobulin homology							
C;Keywords: heterotrimer; immunoglobulin F;32-115/Domain: immunoglobulin homology <1MM>							
Query Match 88 2%; Score 548; DB 2; Length 139;							
Best Local Similarity 86.9%; Pred. No. 1.9e-44;							
Matches 106; Conservative 2; Mismatches 8; Indels 6; Gaps 1;							
Qy 1 EVQLVQSGAEVKPKGESSLR1.....TRGDRGVDYWQQGTIVTVSS 116							
Db 18 EVQLVQSGAEVKPKGESSLR1.....TRGDRGVDYWQQGTIVTVSS 116							
Qy 61 SPSFQQVTISADKS1STAYLQWSLKS1ASDTSAMYCTRG-----DRGVDTWQQGTIVTV 114							
Db 78 SPSFQQVTISADKS1STAYLQWSLKS1ASDTSAMYCARSISSGGYSNFDWQQGTIVTV 137							
RESULT 2							
PH1428	19 heavy chain V region (clone VH5-1R1) - human (fragment)						
C;Species: Homo sapiens (man)							
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 28-May-1999							
C;Accession: PH1428							
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.							
J;Exp. Med. 177, 99-107, 1993							
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of dermatitis.							
A;Reference number: PH1409; PMID:93115676; PMID:8418213							
A;Molecule type: mRNA							
A;Residues: 1-113 <VNAN>							
A;Cross-references: UNIPARC:UPI0000176877; GB:SS1905; NID:9262690; PID: AAC80261.1; PMID: 10793							
C;Superfamily: immunoglobulin V region; immunoglobulin homology							
C;Keywords: heterotrimer; immunoglobulin							

P;15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 543.5; DB 2; Length 113;
Best Local Similarity 89.7%; Pred. No. 4e-44;
Matches 104; Conservative 3; Mismatches 6; Indels 3; Gaps 1;

Qy 1 EVQLVQSAEVKKPGESLIRISCKGSDFSFYIGWVRQMPGKGLEMMGIIYPGSDTIV 60
Db 1 EVQLVQSAEVKKPGESLIRISCKGSDFSFYIGWVRQMPGKGLEMMGIIYPGSDTIV 60

Qy 61 SPSFQQVTISADKSISTAYLQNSLKAQDTAMYCTRDGRGYDYGQGTLYVSS 116
Db 61 SPSFQQVTISADKSISTAYLQNSLKAQDTAMYCTRDGRGYDYGQGTLYVSS 116

Qy 61 SPSFQQVTISADKSISTAYLQNSLKAQDTAMYCTRDGRGYDYGQGTLYVSS 116
Db 61 SPSFQQVTISADKSISTAYLQNSLKAQDTAMYCA--RAFDWQGIMVTVSS 113

RESULT 5

C3606 Ig heavy chain V region (83D2) - human

C:Species: Homo sapiens (man)
C:Accession: C3606
C:Cross-references: 21-Dec-1990 #text_change 16-Dec-1998

R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A38005; PMID:90349571; PMID:2117273

A;Accession: C3606
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-123 <SCH>
A;Cross-references: UNIPARC:UPI0000176C49; GB:M34022
C;Genetics:
A;Gene: GDB:IGH@; IGHDY1
A;Cross-references: GDB:IGH@; OMIM:146910

A;Map position: 14q32.33-14q32.33

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.4%; Score 536.5; DB 2; Length 123;
Best Local Similarity 84.6%; Pred. No. 2e-43;
Matches 104; Conservative 4; Mismatches 8; Indels 7; Gaps 1;

Qy 1 EVQLVQSAEVKKPGESLIRISCKGSDFSFYIGWVRQMPGKGLEMMGIIYPGSDTIV 60
Db 1 EVQLVQSAEVKKPGESLIRISCKGSDFSFYIGWVRQMPGKGLEMMGIIYPGSDTIV 60

Qy 61 SPSFQQVTISADKSISTAYLQNSLKAQDTAMYCTRDGRGYDYGQGTLYVSS 113
Db 61 SPSFQQVTISADKSISTAYLQNSLKAQDTAMYCTRDGRGYDYGQGTLYVSS 113

Qy 114 VSS 116
Db 121 VSS 123

RESULT 6

A49047 Ig heavy chain V region (monoclonal striational autoantibody STRAB SA-1A VH) - human (fr)

C:Species: Homo sapiens (man)
C:Accession: A49047
C:Cross-references: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998

R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2221-2226, 1992

A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A;Reference number: A49047; PMID:92387224; PMID:1516616
A;Accession: A49047
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-136 <VIC>
A;Cross-references: UNIPARC:UPI0000176C6A

A;Experimental source: thymic B lymphocytes
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 535; DB 2; Length 136;
Best Local Similarity 78.8%; Pred. No. 3.1e-43;

Matches 104; Conservative 4; Mismatches 8; Indels 16; Gaps 1; Best Local Similarity 84.6%; Pred. No. 9.3e-43; Matches 104; Conservative 2; Mismatches 10; Indels 8; Gaps 1; Best Local Similarity 84.6%; Pred. No. 9.3e-43;

Qy 1 EVQLVQSGAEVKPGESLRISCKSGDSFTTYWIGHVRQMPKGLEWMGIYPGDSDTIY 60
 Db 5 EVQLVQSGAEVKPGESLRISCKSGDSFTTYWIGHVRQMPKGLEWMGIYPGDSDTIY 64

Qy 61 SPSFQGVTISADKSISTAYLQWSSLKASDAMYCCTRGD-----RGVD 104
 Db 65 SPSFQGVTISADKSISTAYLQWSSLKASDAMYCARRYSYAQHDWYFDLWGRGLTVT 124

Qy 105 YNGQFLTVVSS 116
 Db 125 VNGEGITVTVVSS 136

Db 121 VSS 123

RESULT 7

S38492 19 heavy chain - human (fragment)
 C; Species: Homo sapiens (man)
 C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C; Accession: S38492 R; Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S submitted to the EMBL Data Library, June 1993

A; Description: Human antibody fragments specific for human blood group antigens from a patient A; Reference number: S38488

A; Accession: S38492 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-123 <MAB>

A; Cross-references: UNIPARC:UPI000011654D; EMBL:223034; NID:9414031; PIDN:CAA80569_1; PI
 C; Superfamily: immunoglobulin V region; immunoglobulin homology
 C; Keywords: heterotetramer; immunoglobulin
 F; 15-98/Domain: immunoglobulin homology <IMM>

Query Match 1 EVQLVQSGAEVKPGESLRISCKSGDSFTTYWIGHVRQMPKGLEWMGIYPGDSDTIY 60
 Best Local Similarity 84.6%; Pred. No. 3.1e-43; Length 123;
 Matches 104; Conservative 4; Mismatches 8; Indels 7; Gaps 1;

Qy 1 QVQLVQSGAEVKPGESLRISCKSGDSFTTYWIGHVRQMPKGLEWMGIYPGDSDTIY 60
 Db 1 SPSFQGVTISADKSISTAYLQWSSLKASDAMYCCTRGD-----GDRGYDYGQGTLYT 113

Qy 61 SPSFQGVTISADKSISTAYLQWSSLKASDAMYCARRYSYAQHDWYFDLWGRGLTVT 120
 Db 61 SPSFQGVTISADKSISTAYLQWSSLKASDAMYCARRYSYAQHDWYFDLWGRGLTVT 120

Qy 114 VSS 116
 Db 121 VSS 123

RESULT 9

PH1413 Ig heavy chain V region (clone P1-56) - human (fragment)
 C; Species: Homo sapiens (man)
 C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000

C; Accession: PH1413 R; van der Stoep, N.; van der Linden, J.; Logtenberg, T.
 J. Exp. Med. 177, 99-107, 1993

A; Title: Molecular evolution of the human immunoglobulin E response: High incidence of dermatitis.
 A; Reference number: PH1409; MUID:93115676; PMID:8418213

A; Molecule type: mRNA
 A; Residues: 1-123 <VAN>

A; Cross-references: UNIPARC:UPI0000176A34
 A; Experimental source: PBMC
 A; Note: The authors translated the codon CTG for residue 115 as Met

C; Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
 C; Keywords: heterotetramer; immunoglobulin
 F; 15-98/Domain: immunoglobulin homology <IMM>

Query Match 1 EVQLVQSGAEVKPGESLRISCKSGDSFTTYWIGHVRQMPKGLEWMGIYPGDSDTIY 60
 Best Local Similarity 84.6%; Pred. No. 2.1e-42; Length 123;
 Matches 100; Conservative 6; Mismatches 6; Indels 10; Gaps 3;

Qy 1 EVQLVQSGAEVKPGESLRISCKSGDSFTTYWIGHVRQMPKGLEWMGIYPGDSDTIY 60
 Db 1 SPSFQGVTISADKSISTAYLQWSSLKASDAMYCARRYSYAQHDWYFDLWGRGLTVT 113

Qy 61 SPSFQGVTISADKSISTAYLQWSSLKASDAMYCARRYSYAQHDWYFDLWGRGLTVT 120
 Db 61 SPSFQGVTISADKSISTAYLQWSSLKASDAMYCARRYSYAQHDWYFDLWGRGLTVT 120

Qy 114 VSS 116
 Db 121 VSS 123

RESULT 8

PH1415 Ig heavy chain V region (clone P1-53) - human (fragment)
 C; Species: Homo sapiens (man)
 C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000

C; Accession: PH1415 R; van der Stoep, N.; van der Linden, J.; Logtenberg, T.
 J. Exp. Med. 177, 99-107, 1993

A; Title: Molecular evolution of the human immunoglobulin E response: High incidence of dermatitis.
 A; Reference number: PH1409; MUID:93115676; PMID:8418213

A; Molecule type: mRNA
 A; Residues: 1-127 <VAN>

A; Cross-references: UNIPARC:UPI0000176A12
 A; Experimental source: PBMC
 A; Note: The authors translated the codon TTG for residue 118 as Met

C; Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
 F; 15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 529.5; DB 2; Length 127;
 Best Local Similarity 82.1%; Pred. No. 2.2e-42; Mismatches 6; Indels 7; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGEISLIRISCKGSDFSTTYWIGVRQMPGKLEMGGIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGEISLIRISCKGSDFSTTYWIGVRQMPGKLEMGGIYPGDSDTIY 60
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1423
R;van der Stoop, N.; van der Linden, J.; Logtenberg, T.
J.; Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Molecule type: mRNA
A;Residues: 1-123 <VAN>
A;Cross-references: UNIPARC:UPI0000176B98
A;Experimental source: PBMC
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin Fc15/98/Domain: immunoglobulin homology <IMM>

Query Match Score 524.5%; DB 2; Length 123;
Best Local Similarity 84.5%; Pred. No. 2.6e-42;
Matches 102; Conservative 3; Mismatches 11; Indels 3; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGEISLIRISCKGSDFSTTYWIGVRQMPGKLEMGGIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGEISLIRISCKGSDFSTTYWIGVRQMPGKLEMGGIYPGDSDTIY 60
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1420
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J.; Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Molecule type: mRNA
A;Residues: 1-134 <VAN>
A;Cross-references: UNIPARC:UPI0000176A2E
A;Experimental source: PBMC
A;Note: the authors translated the codon ARG for residue 93 as Thr
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin Fc15/98/Domain: immunoglobulin homology <IMM>

Query Match Score 83.7%; DB 2; Length 134;
Best Local Similarity 83.7%; Pred. No. 7.7e-42;
Matches 103; Conservative 2; Mismatches 11; Indels 14; Gaps 2;

Qy 1 EVQLVQSGAEVKKPGEISLIRISCKGSDFSTTYWIGVRQMPGKLEMGGIYPGDSDTIY 60

Matches 101; Conservative 6; Mismatches 9; Indels 7; Gaps 2;
 Qy 1 EVQLVQSGAEVKKPGESSLRISCKGSQDSFTTYWIGVRQMPGKGLEWMGIIYPGDSDTIY 60
 Db 1 EVQLVQSGAEVKKPGESSLRISCKGSQDSFTTYWIGVRQMPGKGLEWMGIIYPGDSDTIY 60

Qy 61 SPSFQGQTISADKSISTAYLQWSSLKASDTSAMYCTR-GDRGV----DYWGQGTIYT 113
 Db 61 SPSFQGQTISADKSISTAYLQWSSLKASDTSAMYCTR-GDRGV----DYWGQGTIYT 113

Qy 114 VSS 116
 Db 121 VPS 123

RESULT 15

S19669
 19 heavy chain V region (VH5DJ) - human
 C;Species: Homo sapiens (man)
 C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
 C;Accession: S19669
 R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J.; Mol. Biol. 22, 581-591, 1991
 A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage
 A;Reference number: S19663; MUID:92085276; PMID:1748994
 A;Accession: S19669
 A;Molecule type: mRNA
 A;Residues: 1-117 <MAR>
 A;Cross-references: UNIPARC:UPI000115PEA; EMBL:X61651; NID:937731; PIDN:CNA43832.1; PIDC
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.7%; Score 513 5; DB 2; Length 117;
 Best Local Similarity 83.8%; Pred. No. 2.7e-41;
 Matches 98; Conservative 7; Mismatches 11; Indels 1; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESSLRISCKGSQDSFTTYWIGVRQMPGKGLEWMGIIYPGDSDTIY 60
 Db 1 QVQLVQSGAEVKKPGESSLRISCKGSQDSFTTYWIGVRQMPGKGLEWMGIIYPGDSDTIY 60

Qy 61 SPSFQGQTISADKSISTAYLQWSSLKASDTSAMYCTR-GDRGV-DYWQGTIYT 116
 Db 61 SPSFEGQTISVDSITLWSSLKASDTSAMYCTR-GDRGV-DYWQGTIYT 117

Search completed: December 3, 2005, 14:33:32
 Job time : 32.7225 secs

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OM protein - protein search, using SW model

Run on: December 3, 2005, 13:27:13 ; Search time 159.086 Seconds

304.667 Million cell updates/sec

Title: US-10-769-144-4

Perfect score: 621

Sequence: 1 EVQLVQSGAEVKPGESELRI.....TRGDRGVYDWMQQGTIVTSS 116

Scoring table: BLOSUM62

Gapp 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen Parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

Database : Published Applications AA_Main:*

1: /cgns_6/prodata/1/pubpaal/us07_pubcomb.dep:
2: /cgns_6/prodata/1/pubpaal/us08_pubcomb.dep:
3: /cgns_6/prodata/1/pubpaal/us09_pubcomb.dep:
4: /cgns_6/prodata/1/pubpaal/us10_pubcomb.dep:
5: /cgns_6/prodata/1/pubpaal/us10_pubcomb.dep:
6: /cgns_6/prodata/1/pubpaal/us11_pubcomb.dep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	621	100.0	116	3	US-09-651-614-4	Sequence 4, Appli
2	621	100.0	116	4	US-10-035-631-4	Sequence 4, Appli
3	621	100.0	116	5	US-10-769-144-4	Sequence 4, Appli
4	621	100.0	116	5	US-10-903-191-4	Sequence 4, Appli
5	621	100.0	411	5	US-10-769-144-12	Sequence 12, Appli
6	621	100.0	411	5	US-10-903-191-12	Sequence 12, Appli
7	621	100.0	468	5	US-10-769-144-2	Sequence 2, Appli
8	621	100.0	468	5	US-10-903-191-2	Sequence 2, Appli
9	621	100.0	613	5	US-10-769-144-10	Sequence 10, Appli
10	621	100.0	613	5	US-10-903-191-10	Sequence 10, Appli
11	560	90.2	117	5	US-10-726-332-138	Sequence 138, Appli
12	558	89.9	117	5	US-10-726-332-9	Sequence 9, Appli
13	556	89.5	120	4	US-10-956-191-6	Sequence 6, Appli
14	556	89.5	120	5	US-10-956-191-6	Sequence 6, Appli
15	552.5	89.0	252	3	US-09-880-748-1537	Sequence 1537, Appli
16	552.5	89.0	252	4	US-10-233-418-1537	Sequence 144, Appli
17	552.5	88.9	117	5	US-10-726-332-145	Sequence 145, Appli
18	550.5	88.6	118	5	US-10-726-332-145	Sequence 145, Appli
19	550	88.6	224	4	US-10-128-520-167	Sequence 167, Appli
20	550	88.6	224	4	US-10-128-520-170	Sequence 170, Appli
21	548.5	88.6	226	4	US-10-128-520-159	Sequence 159, Appli
22	548.5	88.3	118	5	US-10-726-332-31	Sequence 31, Appli
23	548.5	88.3	118	5	US-10-726-332-134	Sequence 134, Appli
24	548.5	88.3	138	4	US-10-395-894-27	Sequence 27, Appli
25	548.5	88.3	138	4	US-10-693-667-27	Sequence 27, Appli
26	548.5	88.3	138	5	US-10-976-352-27	Sequence 27, Appli
27	548	88.2	224	4	US-10-128-520-165	Sequence 165, Appli

ALIGNMENTS

RESULT 1
US-09-851-614-4
; Sequence 4, Application US/0951614
; Publication No. US2003016702A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC CELLS
; FILE REFERENCE: MXI-166
; CURRENT APPLICATION NUMBER: US/09/851, 614
; CURRENT FILING DATE: 2001-05-08
; PRIORITY APPLICATION NUMBER: USN 60/233, 126
; PRIORITY FILING DATE: 2000-05-08
; PRIORITY APPLICATION NUMBER: USN 60/230, 739
; PRIORITY FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 116
TYPE: PRT
ORGANISM: Homo sapiens
US-09-851-614-4

Query Match 100.0%; Score 621; DB 3;
Best Local Similarity 100.0%; Pred. No. 8.2e-49;
Matchers 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVSGAELYKPKGSLSRISCKGSDFSFTYWIGVROMPGKGIEWMGITYPGGSDDTIY 60
Db 1 EVQLVSGAELYKPKGSLSRISCKGSDFSFTYWIGVROMPGKGIEWMGITYPGGSDDTIY 60
Qy 61 SPSFQQVTISADKSISTAYLQWSLKAISDTAMYCTRGDRGVDNGQTLTVSS 116
Db 61 SPSFQQVTISADKSISTAYLQWSLKAISDTAMYCTRGDRGVDNGQTLTVSS 116

RESULT 2
US-10-035-637-4
; Sequence 4, Application US/10035637
; Publication No. US2003031667A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keller, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC CELLS
; FILE REFERENCE: MXI-166CP
; CURRENT APPLICATION NUMBER: US/10/035, 637
; CURRENT FILING DATE: 2001-11-07
; PRIORITY APPLICATION NUMBER: 09/851, 614

/ PRIOR FILING DATE: 2001-03-08
 / PRIOR APPLICATION NUMBER: USSN 60/203,126
 / PRIOR FILING DATE: 2000-05-08
 / PRIOR APPLICATION NUMBER: USSN 60/230,739
 / PRIOR FILING DATE: 2000-09-07
 / NUMBER OF SEQ ID NOS: 9
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO: 4
 / LENGTH: 116
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-10-035-637-4

Query Match 100.0%; Score 621; DB 4; Length 116;
 Best Local Similarity 100.0%; Pred. No. 8.2e-49;
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 US-10-903-191-4

Query Match 100.0%; Score 621; DB 5; Length 116;
 Best Local Similarity 100.0%; Pred. No. 8.2e-49;
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLYSGAEVKKPGESLRISCKGSDFSTTYWIGVRQMPGKGLEWMGGIYPGDSDTY 60
 Db 1 EVQLYSGAEVKKPGESLRISCKGSDFSTTYWIGVRQMPGKGLEWMGGIYPGDSDTY 60

Qy 61 SPSFQQVTISADKS1STAYLQWSSLIKASDAMYTCTRGDRGVDTWGGTLYTVSS 116
 Db 61 SPSFQQVTISADKS1STAYLQWSSLIKASDAMYTCTRGDRGVDTWGGTLYTVSS 116

RESULT 3
 US-10-769-144-4
 / Sequence 4, Application US/10769144
 / Publication No. US20040248215A1
 / GENERAL INFORMATION:
 / APPLICANT: Keller, Tibor
 / APPLICANT: He, Lizhen
 / APPLICANT: Ramakrishna, Venky
 / TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
 / TITLE OF INVENTION: THEREFOR
 / FILE REFERENCE: MXI-301
 / CURRENT APPLICATION NUMBER: US/10/769,144
 / CURRENT FILING DATE: 2004-01-30
 / PRIOR APPLICATION NUMBER: 60/443979
 / PRIOR FILING DATE: 2003-01-31
 / NUMBER OF SEQ ID NOS: 32
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO: 4
 / LENGTH: 116
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-10-769-144-4

Query Match 100.0%; Score 621; DB 5; Length 116;
 Best Local Similarity 100.0%; Pred. No. 8.2e-49;
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLYSGAEVKKPGESLRISCKGSDFSTTYWIGVRQMPGKGLEWMGGIYPGDSDTY 60
 Db 1 EVQLYSGAEVKKPGESLRISCKGSDFSTTYWIGVRQMPGKGLEWMGGIYPGDSDTY 60

Qy 61 SPSFQQVTISADKS1STAYLQWSSLIKASDAMYTCTRGDRGVDTWGGTLYTVSS 116
 Db 61 SPSFQQVTISADKS1STAYLQWSSLIKASDAMYTCTRGDRGVDTWGGTLYTVSS 116

RESULT 4
 US-10-903-191-4
 / Sequence 4, Application US/10903191
 / Publication No. US2005180983A1
 / GENERAL INFORMATION:
 / APPLICANT: Keller, Tibor
 / APPLICANT: He, Lizhen
 / APPLICANT: Ramakrishna, Venky
 / TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES

RESULT 5
 US-10-769-144-12
 / Sequence 12, Application US/10769144
 / Publication No. US20040248215A1
 / GENERAL INFORMATION:
 / APPLICANT: Endres, Michael
 / APPLICANT: He, Lizhen
 / APPLICANT: Ramakrishna, Venky
 / TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES

Query Match 100.0%; Score 621; DB 5; Length 411;
 Best Local Similarity 100.0%; Pred. No. 2.9e-48;
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLYSGAEVKKPGESLRISCKGSDFSTTYWIGVRQMPGKGLEWMGGIYPGDSDTY 60
 Db 142 EVQLYSGAEVKKPGESLRISCKGSDFSTTYWIGVRQMPGKGLEWMGGIYPGDSDTY 201

Qy 61 SPSFQQVTISADKS1STAYLQWSSLIKASDAMYTCTRGDRGVDTWGGTLYTVSS 116
 Db 202 SPSFQQVTISADKS1STAYLQWSSLIKASDAMYTCTRGDRGVDTWGGTLYTVSS 257

RESULT 6
 US-10-903-191-12
 / Sequence 12, Application US/10903191
 / Publication No. US2005180983A1
 / GENERAL INFORMATION:
 / APPLICANT: Keller, Tibor
 / APPLICANT: He, Lizhen
 / APPLICANT: Ramakrishna, Venky
 / TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES

APPLICANT: He, Lizhen
 APPLICANT: Ramakrishna, Venky
 TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
 FILE REFERENCE: MXI-301CP
 CURRENT APPLICATION NUMBER: US/10/903,191
 CURRENT FILING DATE: 2004-07-30
 PRIOR APPLICATION NUMBER: 10/769144
 PRIOR FILING DATE: 2004-01-30
 PRIOR APPLICATION NUMBER: 60/443979
 PRIOR FILING DATE: 2003-01-31
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 12
 LENGTH: 411
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-903-191-12

Query Match 100.0%; Score 621; DB 5; Length 411;
 Best Local Similarity 100.0%; Pred. No. 2.9e-48;
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVOLVOSGAEVKPGESLRISCKSGDSFTYIGVRQMPGKGLEWMGIYPGDSPTIY 60
 Db 142 EVOLVOSGAEVKPGESLRISCKSGDSFTYIGVRQMPGKGLEWMGIYPGDSPTIY 201

Qy 61 SPSFQGVTISADKSISTAYLQWSSLKASDAMYCCTRGRGVDTWQGTLYTVSS 116
 Db 202 SPSFQGVTISADKSISTAYLQWSSLKASDAMYCCTRGRGVDTWQGTLYTVSS 257

RESULT 7
 US-10-769-144-2
 Sequence 2, Application US/10769144
 Publication No. US20040248215A1
 GENERAL INFORMATION:
 APPLICANT: Keler, Tibor
 APPLICANT: Endres, Michael
 APPLICANT: He, Lizhen
 APPLICANT: Ramakrishna, Venky
 TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
 FILE REFERENCE: MXI-301
 CURRENT APPLICATION NUMBER: US/10/769,144
 CURRENT FILING DATE: 2004-01-30
 PRIOR APPLICATION NUMBER: 60/443979
 PRIOR FILING DATE: 2003-01-31
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 2
 LENGTH: 468
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-769-144-2

Query Match 100.0%; Score 621; DB 5; Length 468;
 Best Local Similarity 100.0%; Pred. No. 3.3e-48;
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVOLVOSGAEVKPGESLRISCKSGDSFTYIGVRQMPGKGLEWMGIYPGDSPTIY 60
 Db 20 EVOLVOSGAEVKPGESLRISCKSGDSFTYIGVRQMPGKGLEWMGIYPGDSPTIY 79

Qy 61 SPSFQGVTISADKSISTAYLQWSSLKASDAMYCCTRGRGVDTWQGTLYTVSS 116
 Db 80 SPSFQGVTISADKSISTAYLQWSSLKASDAMYCCTRGRGVDTWQGTLYTVSS 135

RESULT 8
 US-10-769-191-2
 Sequence 2, Application US/10903191
 Publication No. US20050160983A1

RESULT 9
 US-10-769-144-10
 Sequence 10, Application US/10769144
 Publication No. US20040248215A1
 GENERAL INFORMATION:
 APPLICANT: Keler, Tibor
 APPLICANT: Endres, Michael
 APPLICANT: He, Lizhen
 APPLICANT: Ramakrishna, Venky
 TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
 FILE REFERENCE: MXI-301
 CURRENT APPLICATION NUMBER: US/10/769,144
 CURRENT FILING DATE: 2004-01-30
 PRIOR APPLICATION NUMBER: 60/443979
 PRIOR FILING DATE: 2003-01-31
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 10
 LENGTH: 613
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-769-144-10

Query Match 100.0%; Score 621; DB 5; Length 613;
 Best Local Similarity 100.0%; Pred. No. 4.2e-48;
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVOLVOSGAEVKPGESLRISCKSGDSFTYIGVRQMPGKGLEWMGIYPGDSPTIY 60
 Db 20 EVOLVOSGAEVKPGESLRISCKSGDSFTYIGVRQMPGKGLEWMGIYPGDSPTIY 79

Qy 61 SPSFQGVTISADKSISTAYLQWSSLKASDAMYCCTRGRGVDTWQGTLYTVSS 116
 Db 80 SPSFQGVTISADKSISTAYLQWSSLKASDAMYCCTRGRGVDTWQGTLYTVSS 135

RESULT 10

US-10-903-191-10
 / Sequence 10, Application US/10903191
 / Publication No. US2005180393A1
 / GENERAL INFORMATION:
 / APPLICANT: Keler, Tibor
 / APPLICANT: Endres, Michael
 / APPLICANT: He, Lizhen
 / APPLICANT: Ramakrishna, Venky
 / TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
 / TITLE OF INVENTION: THEREFOR
 / FILE REFERENCE: MXI-101CP
 / CURRENT APPLICATION NUMBER: US/10/903,191
 / CURRENT FILING DATE: 2004-07-30
 / PRIOR APPLICATION NUMBER: 10/761144
 / PRIOR FILING DATE: 2004-01-30
 / PRIOR APPLICATION NUMBER: 60/443979
 / PRIOR FILING DATE: 2003-01-31
 / NUMBER OF SEQ ID NOS: 32
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO 10
 / LENGTH: 613
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-10-903-191-10

Query Match 100.0%; Score 621; DB 5; Length 613;
 Best Local Similarity 100.0%; Pred. No. 4.2e-48;
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLYSGAEVKKPGESLRISCKGSDFSTYIWGRQMPGKGLEWMGGIYPGDSDTY 60
 Db 20 EVQLYSGAEVKKPGESLRISCKGSDFSTYIWGRQMPGKGLEWMGGIYPGDSDTY 79

Qy 61 SPSFQQTISADKSISTAYLQWSSLKASDAMYCTRGDRGVDTWGGTIVTVSS 116
 Db 80 SPSFQQTISADKSISTAYLQWSSLKASDAMYCTRGDRGVDTWGGTIVTVSS 135

RESULT 11
 US-10-726-332-138
 / Sequence 138, Application US/10726332
 / Publication No. US2005058649A1
 / GENERAL INFORMATION:
 / APPLICANT: Gregory M. Landes
 / APPLICANT: Mary Haak-Frendscho
 / APPLICANT: Ling Chen
 / APPLICANT: Yen-Wah R. Lee
 / APPLICANT: Meina Liang
 / APPLICANT: Xiao Peng
 / APPLICANT: Xiao-Chi Jia
 / APPLICANT: Mark R. Nocerini
 / TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
 / FILE REFERENCE: AGENIX_072A
 / CURRENT APPLICATION NUMBER: US/10/726,332
 / CURRENT FILING DATE: 2003-12-02
 / PRIOR APPLICATION NUMBER: n/a
 / NUMBER OF SEQ ID NOS: 222
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO 9
 / LENGTH: 117
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-10-726-332-9

Query Match 89.9%; Score 558; DB 5; Length 117;
 Best Local Similarity 91.4%; Pred. No. 4.4e-43;
 Matches 106; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 EVQLYSGAEVKKPGESLRISCKGSDFSTYIWGRQMPGKGLEWMGGIYPGDSDTY 60
 Db 1 EVQLYSGAEVKKPGESLRISCKGSDFSTYIWGRQMPGKGLEWMGGIYPGDSDTY 60

Qy 61 SPSFQQTISADKSISTAYLQWSSLKASDAMYCTRGDRGVDTWGGTIVTVSS 116
 Db 61 SPSFQQTISADKSISTAYLQWSSLKASDAMYCTRGDRGVDTWGGTIVTVSS 116

RESULT 12
 US-10-726-332-9
 / Sequence 9, Application US/10726332
 / Publication No. US2005058649A1
 / GENERAL INFORMATION:
 / APPLICANT: Gregory M. Landes
 / APPLICANT: Mary Haak-Frendscho
 / APPLICANT: Ling Chen
 / APPLICANT: Yen-Wah R. Lee
 / APPLICANT: Meina Liang
 / APPLICANT: Xiao Peng
 / APPLICANT: Xiao-Chi Jia
 / APPLICANT: Mark R. Nocerini
 / TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
 / FILE REFERENCE: AGENIX_072A
 / CURRENT APPLICATION NUMBER: US/10/726,332
 / CURRENT FILING DATE: 2003-12-02
 / PRIOR APPLICATION NUMBER: n/a
 / NUMBER OF SEQ ID NOS: 222
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO 9
 / LENGTH: 117
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-10-726-332-9

Query Match 89.9%; Score 558; DB 5; Length 117;
 Best Local Similarity 91.4%; Pred. No. 2.9e-43;
 Matches 102; Mismatches 8; Indels 0; Gaps 0;

RESULT 13
 US-10-125-687-6
 / Sequence 6, Application US/10125687
 / Publication No. US2005054407A1
 / GENERAL INFORMATION:
 / APPLICANT: Iuqo, Peter
 / TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
 / FILE REFERENCE: 26050-705
 / CURRENT APPLICATION NUMBER: US/10/125,687
 / CURRENT FILING DATE: 2002-04-17
 / PRIOR APPLICATION NUMBER: 2002-04-17
 / NUMBER OF SEQ ID NOS: 28
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 6
 / LENGTH: 120
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / NAME/KEY: VARIANT
 / LOCATION: 99, 100, 102
 / OTHER INFORMATION: Xaa = Any Amino Acid
 US-10-125-687-6

Query Match 90.2%; Score 560; DB 5; Length 117;
 Best Local Similarity 91.4%; Pred. No. 2.9e-43;
 Matches 102; Mismatches 8; Indels 0; Gaps 0;

Query Match 89.5%; Score 556; DB 4; Length 120;
 Best Local Similarity 89.2%; Pred. No. 6.9e-43;

Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;
 Query 1 EVQLVQSGAEVKPGESLRISCKSGSDSFITYWIGVRQMPGKGLIEWMGIYPGDSDTIV 60
 Database 1 EVQLVQSGAEVKPGESLRISCKSGSDSFITYWIGVRQMPGKGLIEWMGIYPGDSDTIV 60
 Best Local Similarity 89.0%; Score 552.5; DB 3; Length 252;
 Matches 106; Conservative 4; Mismatches 6; Indels 9; Gaps 1;
 Query 1 EVQLVQSGAEVKPGESLRISCKSGSDSFITYWIGVRQMPGKGLIEWMGIYPGDSDTIV 60
 Database 1 EVQLVQSGAEVKPGESLRISCKSGSDSFITYWIGVRQMPGKGLIEWMGIYPGDSDTIV 60
 SPSEQGVTISADKSISTAYLQWSSLKAISDTAMYCTR---GDRGVYDYGQGTLYVSS 116
 SPSEQGVTISADKSISTAYLQWSSLKAISDTAMYCTR---GDRGVYDYGQGTLYVSS 120
 RESULT 14
 US-10-996-191-6
 Publication No. Application US/1096191
 Publication No. US20050148001A1
 GENERAL INFORMATION:
 APPLICANT: Luo, Peizhi
 TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
 FILE REFERENCE: 26050-705-301
 CURRENT APPLICATION NUMBER: US 10/996,191
 CURRENT FILING DATE: 2004-11-22
 PRIOR APPLICATION NUMBER: US 60/284,407
 PRIOR FILING DATE: 2001-04-17
 PRIOR APPLICATION NUMBER: US 10/125,687
 PRIOR FILING DATE: 2002-04-17
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 6
 LENGTH: 120
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Human consensus antibody heavy chain variable region
 US-10-996-191-6

Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;
 Query Match 89.5%; Score 556; DB 5; Length 120;
 Best Local Similarity 89.2%; Pred. No. 6.9e-43;
 Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;
 Query 1 EVQLVQSGAEVKPGESLRISCKSGSDSFITYWIGVRQMPGKGLIEWMGIYPGDSDTIV 60
 Database 1 EVQLVQSGAEVKPGESLRISCKSGSDSFITYWIGVRQMPGKGLIEWMGIYPGDSDTIV 60
 SPSEQGVTISADKSISTAYLQWSSLKAISDTAMYCTR---GDRGVYDYGQGTLYVSS 116
 SPSEQGVTISADKSISTAYLQWSSLKAISDTAMYCTR---GDRGVYDYGQGTLYVSS 120
 RESULT 15
 US-09-880-748-1537
 Sequence 1537, Application US/09880748
 Publication No. US20030059937A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
 FILE REFERENCE: PFS23
 CURRENT APPLICATION NUMBER: US/09/880-748
 CURRENT FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: 60/212,210
 PRIOR FILING DATE: 2000-06-15
 PRIOR APPLICATION NUMBER: 60/240,816
 PRIOR FILING DATE: 2000-10-17
 PRIOR APPLICATION NUMBER: 60/276,248
 PRIOR FILING DATE: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/277,379
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/293,499
 PRIOR FILING DATE: 2001-05-25
 NUMBER OF SEQ ID NOS: 3239
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1537
 LENGTH: 252
 TYPE: PRT

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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:48:29 ; Search time 6.62857 Seconds
 (without alignments)

83.796 Million cell updates/sec

Title: US-10-769-144-4

Perfect score: 621

Sequence: 1 EQLVQSGAEVKPGESLRI.....TRGDRGVWDYWGQGTLYTSS 116

Scoring table: BL0QUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0\$ Maximum Match 100\$ Listing first 45 summaries

Database : Published Applications AA_New:*

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2: /cgn2_6/podata/1/pubpaas/US06_NEW_PUB.PEP:*

3: /cgn2_6/podata/1/pubpaas/US07_NEW_PUB.PEP:*

4: /cgn2_6/podata/1/pubpaas/US08_NEW_PUB.PEP:*

5: /cgn2_6/podata/1/pubpaas/FCT_NEW_PUB.PEP:*

6: /cgn2_6/podata/1/pubpaas/US10_NEW_PUB.PEP:*

7: /cgn2_6/podata/1/pubpaas/US11_NEW_PUB.PEP:*

8: /cgn2_6/podata/1/pubpaas/US60_NEW_PUB.PEP:*

'Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.'

;

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	552.5	89.0	252	7 US-11-054-515-1537	Sequence 1537, Ap
2	524.5	84.5	249	7 US-11-054-515-1312	Sequence 1312, Ap
3	501	80.7	248	7 US-11-054-515-2088	Sequence 2088, Ap
4	498	80.2	248	7 US-11-054-515-1	Sequence 1, Appl
5	495	79.8	248	7 US-11-054-515-1995	Sequence 1995, Ap
6	495	79.7	98	7 US-11-054-663-45	Sequence 45, Appl
7	495	79.7	98	7 US-11-084-554-56	Sequence 56, Appl
8	475.5	76.6	249	7 US-11-054-515-1957	Sequence 1957, Ap
9	470.5	75.8	247	7 US-11-054-515-2103	Sequence 2103, Ap
10	447.5	72.1	119	7 US-11-054-669-124	Sequence 124, Ap
11	420.5	67.7	257	7 US-11-054-515-1514	Sequence 1514, Ap
12	408.5	65.8	125	7 US-11-056-074-58	Sequence 58, Appl
13	399.5	64.3	121	7 US-11-108-135-24	Sequence 24, Appl
14	396	63.8	245	7 US-11-054-515-1919	Sequence 1919, Ap
15	395	63.6	238	7 US-11-054-515-1907	Sequence 1907, Ap
16	394	63.4	122	7 US-11-105-268-29	Sequence 29, Appl
17	394	63.4	250	7 US-11-054-515-2097	Sequence 2097, Ap
18	394	63.4	251	7 US-11-054-515-2001	Sequence 2001, Ap
19	392	63.1	116	7 US-11-056-074-50	Sequence 50, Appl
20	392	63.1	242	7 US-11-054-515-2084	Sequence 2084, Appl
21	392	63.1	251	7 US-11-054-515-1592	Sequence 1592, Ap
22	391.5	63.0	117	7 US-11-054-669-120	Sequence 120, Ap
23	390.5	62.9	248	7 US-11-054-515-1104	Sequence 1104, Ap
24	390	62.8	247	7 US-11-056-825-8	Sequence 8, Appl
25	390	62.8	248	7 US-11-054-515-1955	Sequence 1955, Ap

RESULT 1
 US-11-054-515-1537
 ; Sequence 1537, Application US/11054515
 ; Publication No. US2005025532A1
 ; GENERAL INFORMATION:
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523P3
 ; CURRENT APPLICATION NUMBER: US/11/054,515
 ; CURRENT FILING DATE: 2005-02-10
 ; PRIOR APPLICATION NUMBER: 60/543,296
 ; PRIOR FILING DATE: 2004-02-11
 ; PRIOR APPLICATION NUMBER: 60/580,347
 ; PRIOR FILING DATE: 2004-06-18
 ; PRIOR APPLICATION NUMBER: 10/293,418
 ; PRIOR FILING DATE: 2002-11-14
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; Remaining Prior Application data removed - See File Wrapper or PAM.
 ; NUMBER OF SEQ ID NOS: 3247
 ; SEQ ID NO: 1537
 ; LENGTH: 252
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-054-515-1537

Query Match 89%; Score 552.5; DB 7; Length 252;
 Best Local Similarity 84.8%; Pred. No. 8.1e-50;
 Matches 106; Conservative 4; Mismatches 6; Indels 9; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISKGSDDSFPTWYIGVROMPGKGLEWMGILYPGDSPTIY 60
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 1 QVQLVQSGAEVKKPGESLRISKGSDDSFPTWYIGVROMPGKGLEWMGILYPGDSPTIY 60

Db 1 SPSFGQGVYTISADKISTAYLQWSLSKAASDAMYCTRGD-----RGVDYNGQTL 111
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 61 SPSFQQVTTISADKSISTAYLQWSSLKASDTAMYCARLYDILTGYYPSGFDFYWGQ3TM 120
 Qy 112 VTVSS 116
 Db 121 VTVSS 125

RESULT 2

US-11-054-515-1312

Sequence 1312, Application US/11054515

Publication No. US20050255532A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PFS2P3

CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543,296

PRIOR FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: 60/580,347

PRIOR FILING DATE: 2004-06-18

PRIOR APPLICATION NUMBER: 10/293,418

PRIOR FILING DATE: 2002-11-14

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 3247

SEQ ID NO: 2088

LENGTH: 248

TYPE: PRT

ORGANISM: Homo sapiens

US-11-054-515-2088

Query Match 84.5%; Score 524.5; DB 7; Length 249;
 Best Local Similarity 81.6%; Pred. No. 5..6e-47;
 Matches 102; Conservative 5; Missmatches 9; Indels 9; Gaps 1;

SEQ ID NO: 1312

LENGTH: 249

TYPE: PRT

ORGANISM: Homo sapiens

US-11-054-515-1312

Query Match 84.5%; Score 524.5; DB 7; Length 249;
 Best Local Similarity 81.6%; Pred. No. 5..6e-47;
 Matches 102; Conservative 5; Missmatches 9; Indels 9; Gaps 1;

SEQ ID NO: 1312

LENGTH: 249

TYPE: PRT

ORGANISM: Homo sapiens

US-11-054-515-2088

Sequence 2088, Application US/11054515

Publication No. US20050255532A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PFS2P3

CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543,296

PRIOR FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/2088

PRIOR FILING DATE: 2000-10-17
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 3247

SEQ ID NO 1
 LENGTH: 248
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-054 515-1

Query Match 80.2%; Score 49B; DB 7; Length 248;
 Best Local Similarity 76.2%; Pred. No. 2.7e-44;
 Matches 93; Conservative 11; Mismatches 12; Indels 6; Gaps 1;

Qy 1 EVQLVSGAELYKKPGESLRISCKGSGDSFTTYWIGVRQMPGKGLIEWMGIIYPGDSDTIY 60
 Db 1 QVQLQSAELKKPGQLSKLISKCGSCTFTTYWIGVRQLPKGKGLIEWMGIIYPGDSHTY 60

Qy 61 SPSFQGVITISADKSISTAYLQWSLIKASDAMYCCTRDRGV-----DWGQQTLYTV 114
 Db 61 SPSFEGHVNIVSDKSINTAYLQWSLIKASDAMYCARHDDVLTGYYFSWQGQTMVTY 120

Qy 115 SS 116
 Db 121 SS 122

RESULT 5
 US-11-054 515-1995
 Sequence 1995, Application US/11054515
 Publication No. US20050255532A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 FILE REFERENCE: PF523P3
 CURRENT APPLICATION NUMBER: US/11/054,515
 PRIOR APPLICATION NUMBER: 60/543,296
 PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: 60/580,347
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 10/293,418
 PRIOR APPLICATION NUMBER: 60/331,469
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/340,817
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 09/880,748
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: 60/293,499
 PRIOR FILING DATE: 2001-05-15
 PRIOR APPLICATION NUMBER: 60/277,379
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/276,248
 PRIOR FILING DATE: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/240,816
 PRIOR FILING DATE: 2000-10-17
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 3247
 SEQ ID NO 1995
 LENGTH: 248
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-054 515-1995

Query Match 79.8%; Score 495.5; DB 7; Length 248;
 Best Local Similarity 79.7%; Pred. No. 4.9e-14;
 Matches 98; Conservative 6; Mismatches 12; Indels 7; Gaps 2;

Qy 1 EVOLVSGAEVVKPGESLRISCKGSGDSFTTYWIGVRQMPGKGLIEWMGIIYPGDSDTIY 60
 Db 1 EVQLVSGAEVVKPGESLRISCKGSGDSFTTYWIGVRQMPGKGLQUMGIYPGDSSETIY 60

RESULT 6
 US-11-054 669-45
 Sequence 45, Application US/11054669
 Publication No. US20050261480A1
 GENERAL INFORMATION:
 APPLICANT: Foote, Jefferson
 TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
 FILE REFERENCE: 30219/US/3
 CURRENT APPLICATION NUMBER: US/11/054,669
 CURRENT FILING DATE: 2005-02-08
 PRIOR APPLICATION NUMBER: US 10/194,975
 PRIOR FILING DATE: 2002-07-12
 PRIOR APPLICATION NUMBER: US 60/305,111
 PRIOR FILING DATE: 2001-07-12
 NUMBER OF SEQ ID NOS: 124
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 45
 LENGTH: 98
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-054 669-45

Query Match 79.7%; Score 495; DB 7; Length 98;
 Best Local Similarity 94.9%; Pred. No. 2.1e-44;
 Matches 93; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EVQLVSGAEVVKPGESLRISCKGSGDSFTTYWIGVRQMPGKGLIEWMGIIYPGDSDTIY 60
 Db 1 EVQLVSGAEVVKPGESLRISCKGSGDSFTSYWIGVRQMPGKGLIEWMGIIYPGDSTRY 60

Qy 61 SPSFQGVITISADKSISTAYLQWSLIKASDAMYCCTR 98
 Db 61 SPSFQGVITISADKSISTAYLQWSLIKASDAMYCAR 98

RESULT 7
 US-11-084 554-56
 Sequence 56, Application US/11084554
 Publication No. US20050260579A1
 GENERAL INFORMATION:
 APPLICANT: Kellermann, Sirid-Ai
 APPLICANT: Green, Larry L.
 APPLICANT: Korver, Wouter
 TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
 FILE REFERENCE: AGENIX.100A
 CURRENT APPLICATION NUMBER: US/11/084,554
 CURRENT FILING DATE: 2005-03-17
 PRIOR APPLICATION NUMBER: 60/554,372
 PRIOR FILING DATE: 2004-03-19
 PRIOR APPLICATION NUMBER: 60/554,372
 PRIOR FILING DATE: 2004-05-24
 NUMBER OF SEQ ID NOS: 266
 SOFTWARE: PastSeq for Windows Version 4.0
 SEQ ID NO 56
 LENGTH: 98
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-084 554-56

Query Match 79.7%; Score 495; DB 7; Length 98;
 Best Local Similarity 94.9%; Pred. No. 2.1e-44;
 Matches 93; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EVOLVSGAEVVKPGESLRISCKGSGDSFTTYWIGVRQMPGKGLIEWMGIIYPGDSDTIY 60

Db	1	EVQLVSGAVEVKKGPGESLKSISTAYLQWSSLKASDTAMYCTR	98
Qy	61	SPSFQGQTISADKSISTAYLQWSSLKASDTAMYCTR	98
Db	61	SPSFQGQTISADKSISTAYLQWSSLKASDTAMYCTR	98
RESULT 8			
	US-11-054-515-1957		
	Sequence 1957, Application US/11054515		
	Publication No. US20050255532A1		
	GENERAL INFORMATION:		
	APPLICANT: Ruben et al.		
	TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys		
	FILE REFERENCE: PFS53P3		
	CURRENT APPLICATION NUMBER: US/11/054,515		
	CURRENT FILING DATE: 2005-02-10		
	PRIOR APPLICATION NUMBER: 60/543,296		
	PRIOR FILING DATE: 2004-02-11		
	PRIOR APPLICATION NUMBER: 60/550,347		
	PRIOR FILING DATE: 2004-06-18		
	PRIOR APPLICATION NUMBER: 10/293,418		
	PRIOR FILING DATE: 2002-11-14		
	PRIOR APPLICATION NUMBER: 60/331,469		
	PRIOR FILING DATE: 2001-11-16		
	PRIOR APPLICATION NUMBER: 60/340,817		
	PRIOR FILING DATE: 2001-12-19		
	PRIOR APPLICATION NUMBER: 09/880,748		
	PRIOR FILING DATE: 2001-06-15		
	PRIOR APPLICATION NUMBER: 60/293,499		
	PRIOR FILING DATE: 2001-05-25		
	PRIOR APPLICATION NUMBER: 60/277,379		
	PRIOR FILING DATE: 2001-03-21		
	PRIOR APPLICATION NUMBER: 60/276,248		
	PRIOR FILING DATE: 2001-04-16		
	PRIOR APPLICATION NUMBER: 60/240,816		
	PRIOR FILING DATE: 2000-10-17		
	NUMBER OF SEQ ID NOS: 3247		
	SEQ ID NO 1957		
	LENGTH: 249		
	TYPE: PRT		
	ORGANISM: Homo sapiens		
	US-11-054-515-1957		
RESULT 9			
	US-11-054-515-2103		
	Sequence 2103, Application US/1-054515		
	Publication No. US20050255532A1		
	GENERAL INFORMATION:		
	APPLICANT: Ruben et al.		
	TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys		
	FILE REFERENCE: PFS53P3		
	CURRENT APPLICATION NUMBER: US/11/054,515		
	CURRENT FILING DATE: 2005-02-10		

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; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed
; NUMBER OF SEQ ID NOS: 3247
SEQ ID NO: 2103
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2103

Query Match 75.8%; Score
Best Local Similarity 76.4%; Pred.
Matches 93; Conservative 8; Mi

Qy      1 EVQLVSGAEVKKPGGLRISCKGSS
Db      1 EVQLVSGADYKKPGGLKISCKGSS
Qy      61 SPSFQQVTISADKSISAYLQWSS
Db      61 NPSFQQHVTMVDKSISAYLQWSS
Qy      116 S 116
Db      121 S 121

RESULT 10
US-11-054-669-124
Sequence 124, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
;   APPLICANT: Poote, Jefferson
;   TITLE OF INVENTION: SUPER HUMANIZED A
;   FILE REFERENCE: 10219/US/3
;   CURRENT APPLICATION NUMBER: US/11/054
;   CURRENT FILING DATE: 2005-02-08
;   PRIOR APPLICATION NUMBER: US 10/194,9
;   PRIOR FILING DATE: 2002-07-12
;   PRIOR APPLICATION NUMBER: US 60/305,1
;   PRIOR FILING DATE: 2001-07-12
;   NUMBER OF SEQ ID NOS: 124
;   SOFTWARE: PatentIn version 3.3
SEQ ID NO: 124
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-124

Query Match 72.1%; Score
Best Local Similarity 74.8%; Pred.
Matches 89; Conservative 6; Mi

Qy      1 EVQLVSGAEVKKPGGLRISCKGSS

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Db 1 EVQLQSAEVKPGESLRLSCKTSKTSYGSFTSYNSHWRQMPGKELEWMGAIYPRSQDTIY 60
 Qy 61 SPSFOGVTISADKSISTAYLQWSSLKASDAMTYCTRG--DRGYDNGQGTLYTVSS 116
 :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Db 61 NPSFOGHVTISADSSSTAYLQWSSLKASDAMTYCVRSSYDYDAFAFNCGTLYTVSS 119
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-054-515-1514

RESULT 11
 US-11-054-515-1514, Application US/11054515
 ; Sequence 1514, Application US/11054515
 ; PUBLIC INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLys
 ; FILE REFERENCE: PF523P3
 ; CURRENT APPLICATION NUMBER: US/11/054,515
 ; CURRENT FILING DATE: 2005-02-10
 ; PRIOR APPLICATION NUMBER: 60/543,296
 ; PRIOR FILING DATE: 2004-02-11
 ; PRIOR APPLICATION NUMBER: 60/580,347
 ; PRIOR FILING DATE: 2004-06-18
 ; PRIOR APPLICATION NUMBER: 10/293,418
 ; PRIOR FILING DATE: 2002-11-14
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 3247
 ; SEQ ID NO 1514
 ; LENGTH: 257
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-054-515-1514

Query Match 67.7%; Score 420.5%; DB 7; Length 257;
 Best Local Similarity 65.1%; Pred. No. 2.1e-36;
 Matches 84; Conservative 12; Mismatches 20; Indels 13; Gaps 1;

Db 1 EVQLQSAEVKPGESLRLSCKTSKTSYGSFTSYNSHWRQMPGKELEWMGAIYPRSQDTIY 60
 Qy 61 SPSFOGVTISADKSISTAYLQWSSLKASDAMTYCTRG--DRGYDNGQGTLYVSS 107
 :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Db 61 SPSFOGHVTISADSSSTAYLQWSSLKASDAMTYCVRSSYDYDAFAFNCGTLYTVSS 120
 ; OTHER INFORMATION: Humanized heavy chain variable region
 Qy 108 QCTLTVTVSS 116
 Db 121 QCTLTVTVSS 129

RESULT 12
 US-11-096-074-58
 ; Sequence 58, Application US/11096074
 ; Publication No. US/20050260193A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LIEBERBURG, IVAN
 ; TITLE OF INVENTION: STEROID SPARING AGENTS AND METHODS OF USING SAME
 ; CURRENT FILING NUMBER: US/11/096,074
 ; CURRENT FILING DATE: 2005-04-01
 ; PRIOR APPLICATION NUMBER: 60/558,120

Db 121 \$ 121

RESULT 14

US-11-054-515-1919

Sequence 1919, Application US/11054515

Publication No. US2005025532A1

GENERAL INFORMATION:

APPLICANT: Ruben et al

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PF52:PP3

CURRENT APPLICATION NUMBER: US/11/054, 515

CURRENT FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543, 296

PRIOR FILING DATE: 2004-02-11

PRIOR FILING NUMBER: 60/580, 347

PRIOR FILING DATE: 2004-06-18

PRIOR APPLICATION NUMBER: 10/293, 418

PRIOR FILING DATE: 2004-11-14

PRIOR FILING NUMBER: 60/331, 469

PRIOR FILING DATE: 2001-11-16

PRIOR FILING NUMBER: 60/340, 817

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 09/880, 748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/293, 499

PRIOR FILING DATE: 2001-05-25

PRIOR FILING NUMBER: 60/277, 379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/276, 248

PRIOR FILING DATE: 2001-03-16

PRIOR FILING NUMBER: 60/240, 816

PRIOR FILING DATE: 2000-10-17

Remaining Prior Application data removed - See File Wrapper or PALM.

SEQ ID NO: 1919

LENGTH: 245

TYPE: PRT

ORGANISM: Homo sapiens

US-11-054-515-1919

Query Match 63.8%; Score 396; DB 7; Length 245;

Best Local Similarity 61.5%; Pred. No. 6.2e-34;

Matches 75; Conservative 17; Mismatches 24; Indels 6; Gaps 1;

Qy 1 EVOLVOSGAEVVKPGESLRSCKGSGDSFTIWCWVRQMPGKGLEWMGTYPGDSDTIVY 60

Db 1 EVOLVOSGAEVVKPGESLRSCKGSGDSFTIWCWVRQMPGKGLEWMGTYPGDSDTIVY 60

Qy 61 PSFQQTISADKSISTAYLQWSSLKASDAMYTCTRGRGVDTWGOGLTVYSS 114

Db 61 PSFQQTISADKSISTAYLQWSSLKASDAMYTCTRGRGVDTWGOGLTVYSS 114

Qy 115 SS 116

Db 121 SS 122

RESULT 15

US-11-054-515-1907

Sequence 1907, Application US/11054515

Publication No. US2005025532A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PF52:PP3

CURRENT APPLICATION NUMBER: US/11/054, 515

CURRENT FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543, 296

PRIOR FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: 60/580, 347

PRIOR FILING DATE: 2004-06-18

PRIOR APPLICATION NUMBER: 10/293, 418